

FIG. 1A

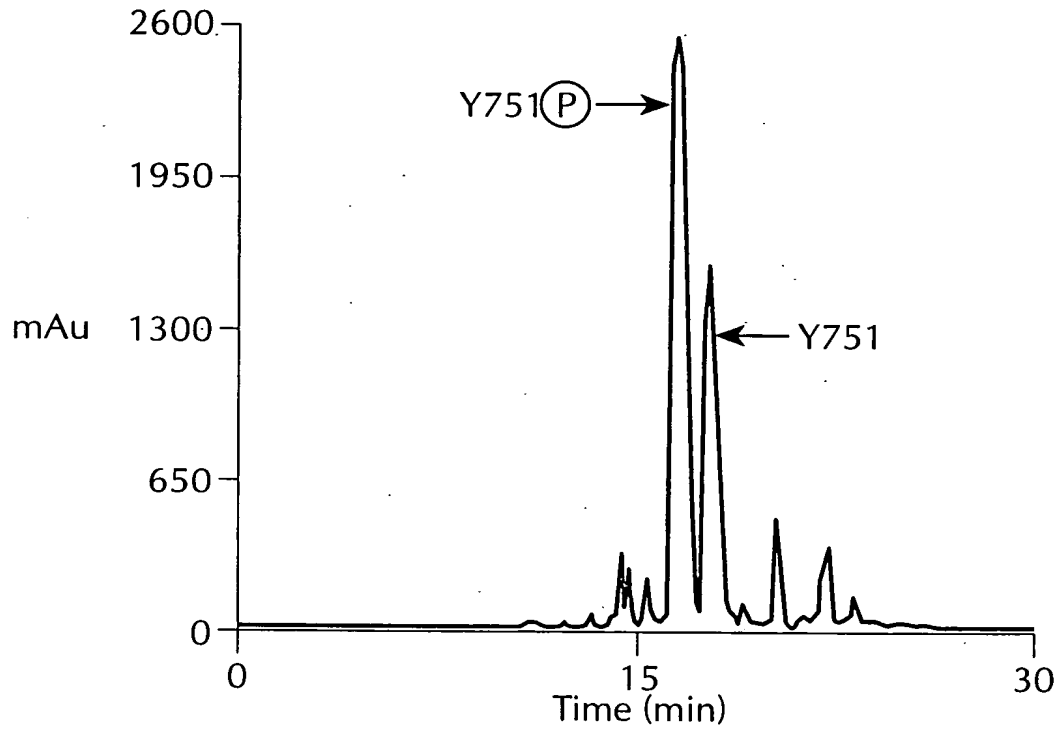


FIG. 1B

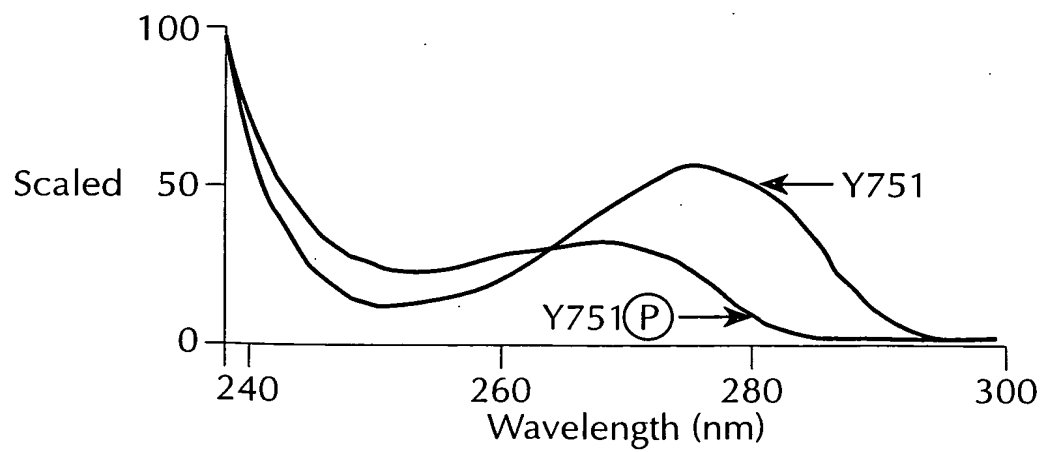


FIG. 1C

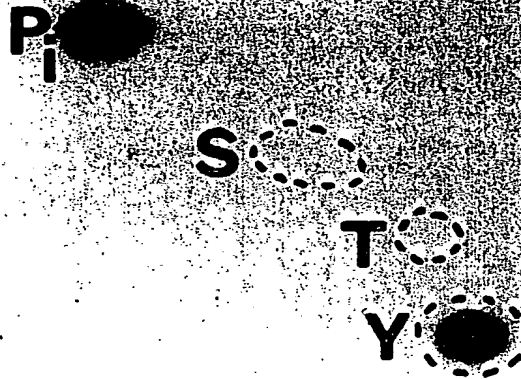


FIG. 1D

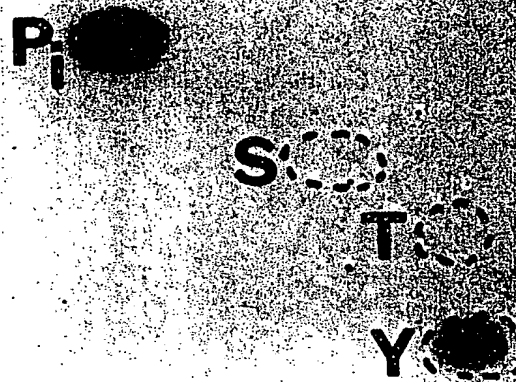


FIG. 2B

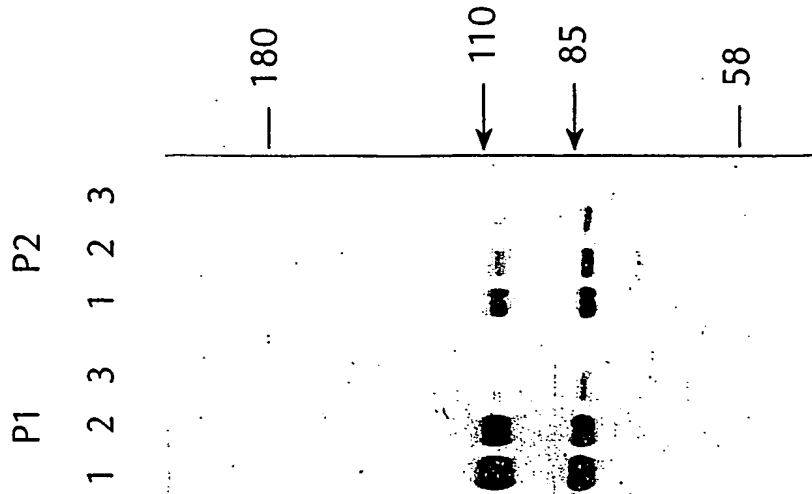


FIG. 2A

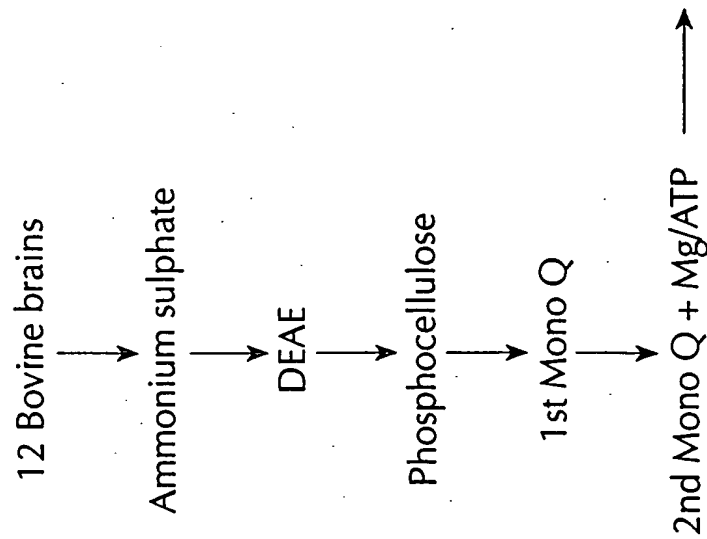
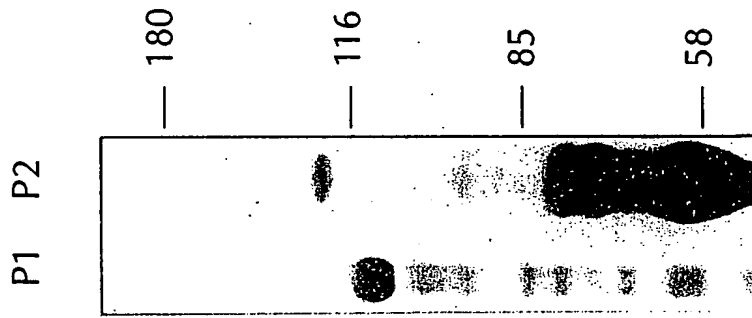


FIG. 3

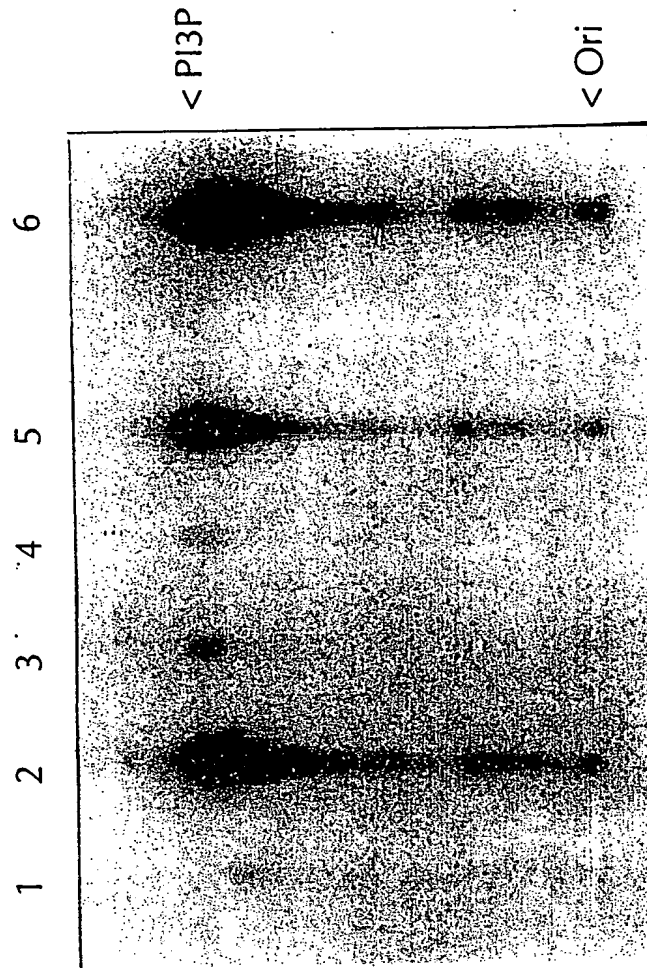


FIG. 4A

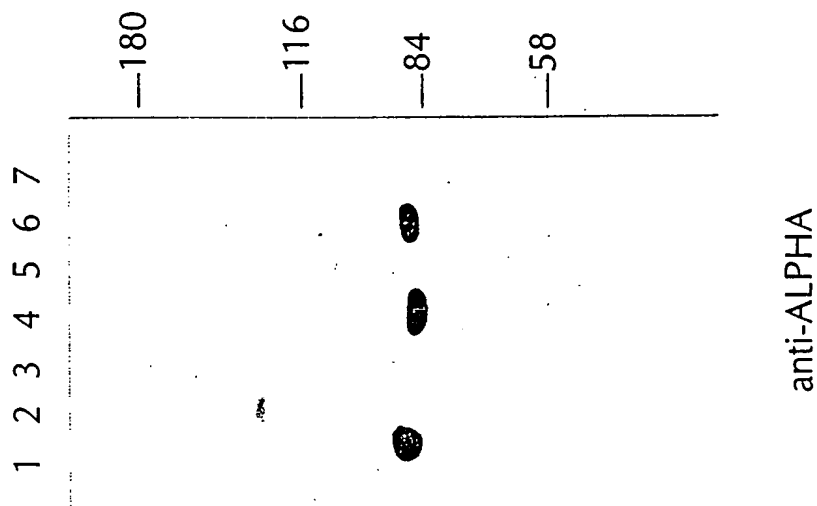


FIG. 4B

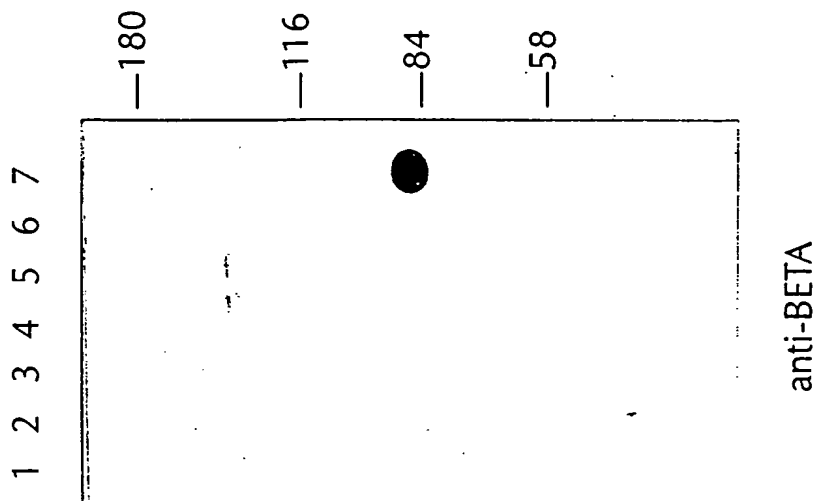


FIG. 4D

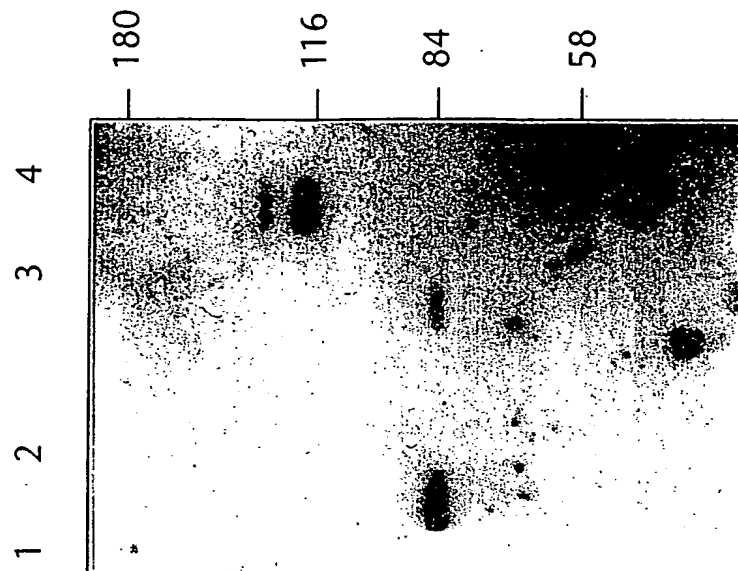


FIG. 4C

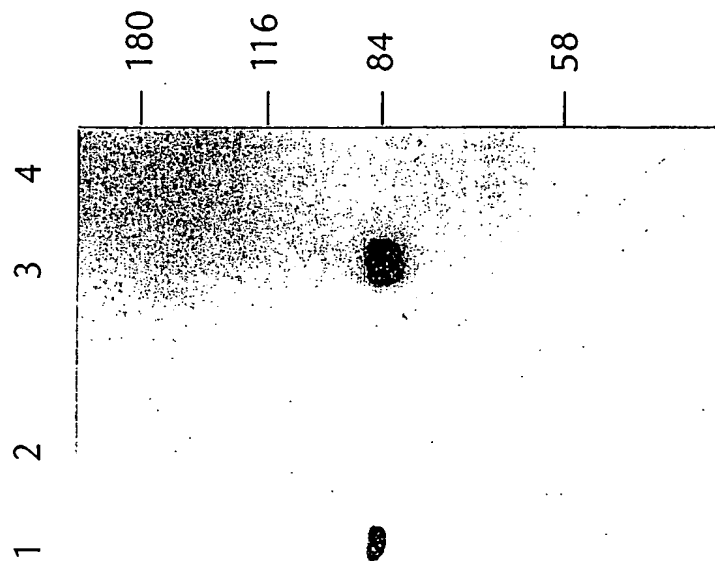


FIG. 5A

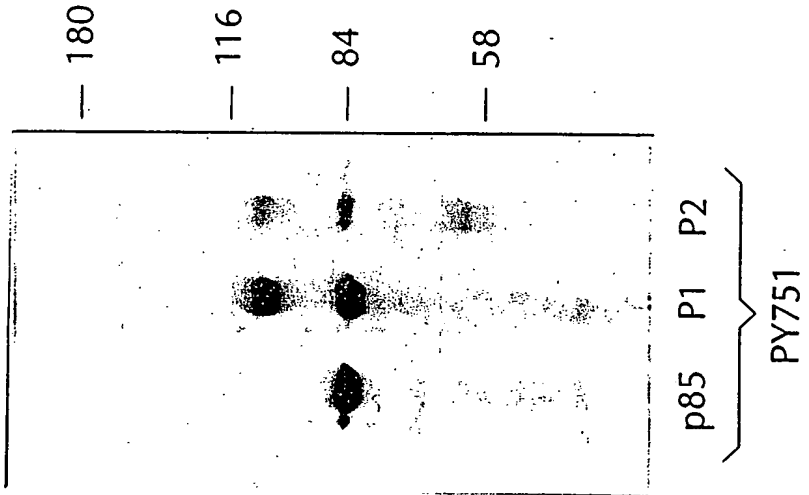


FIG. 5B

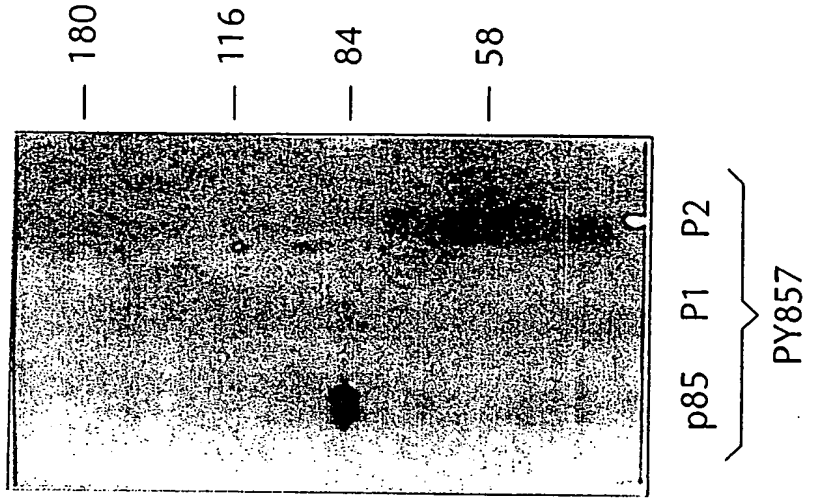


FIG. 6A

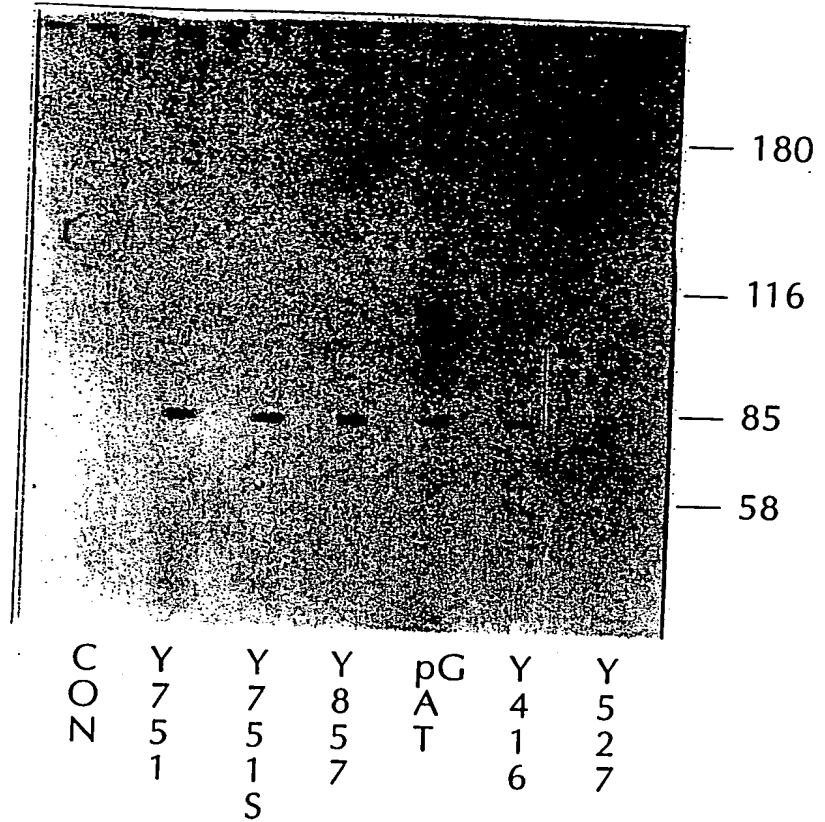


FIG. 6B

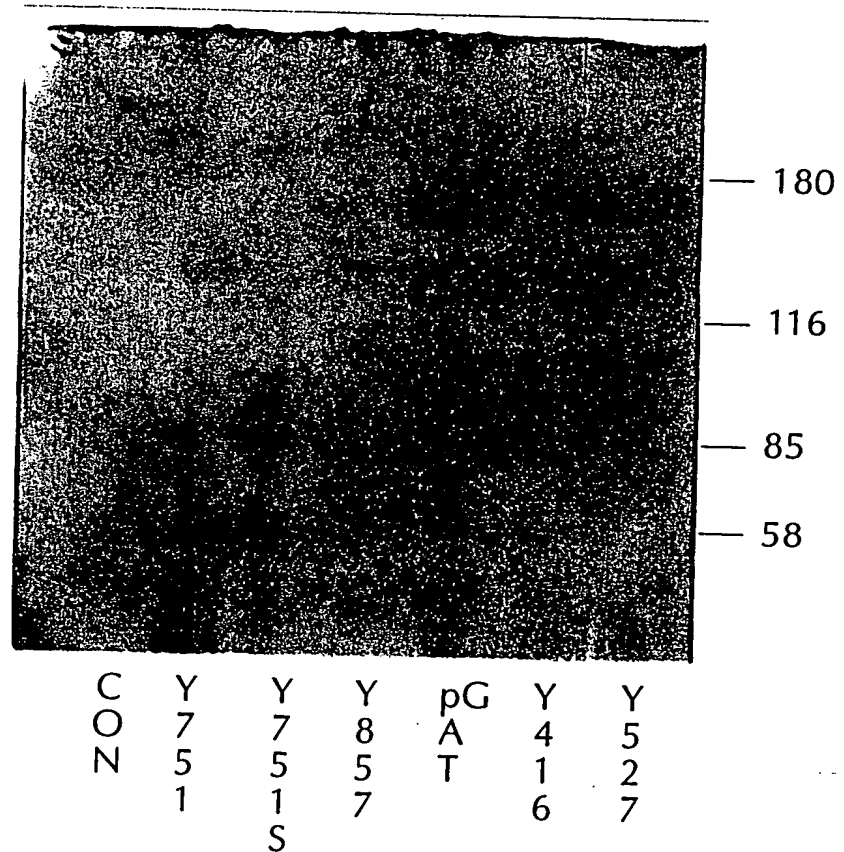


FIG. 7A

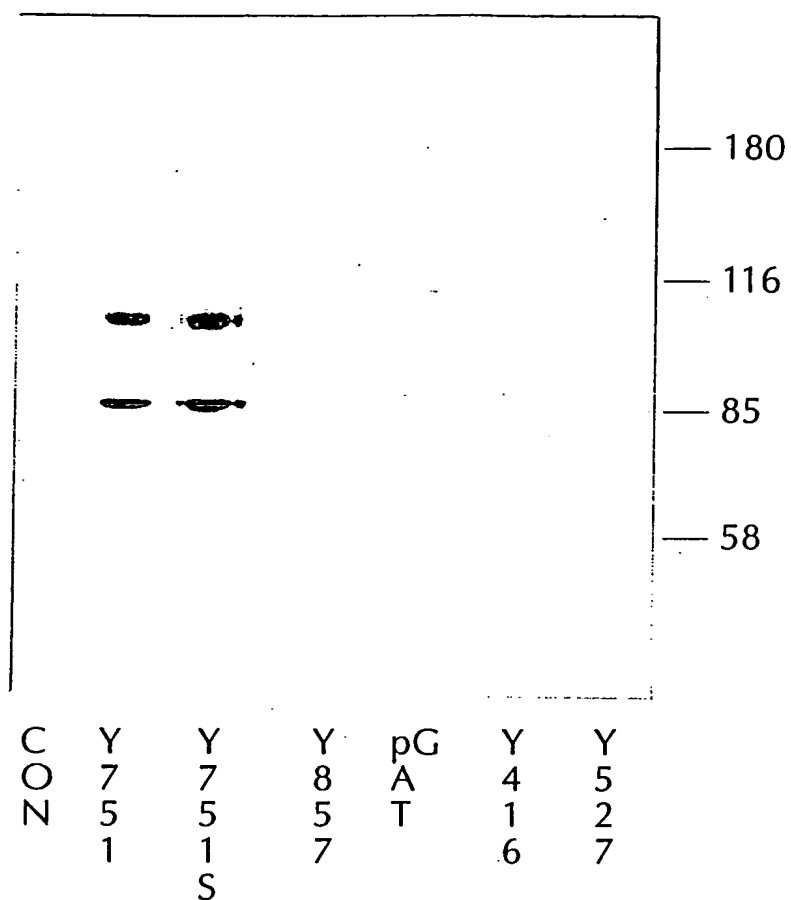


FIG. 7B

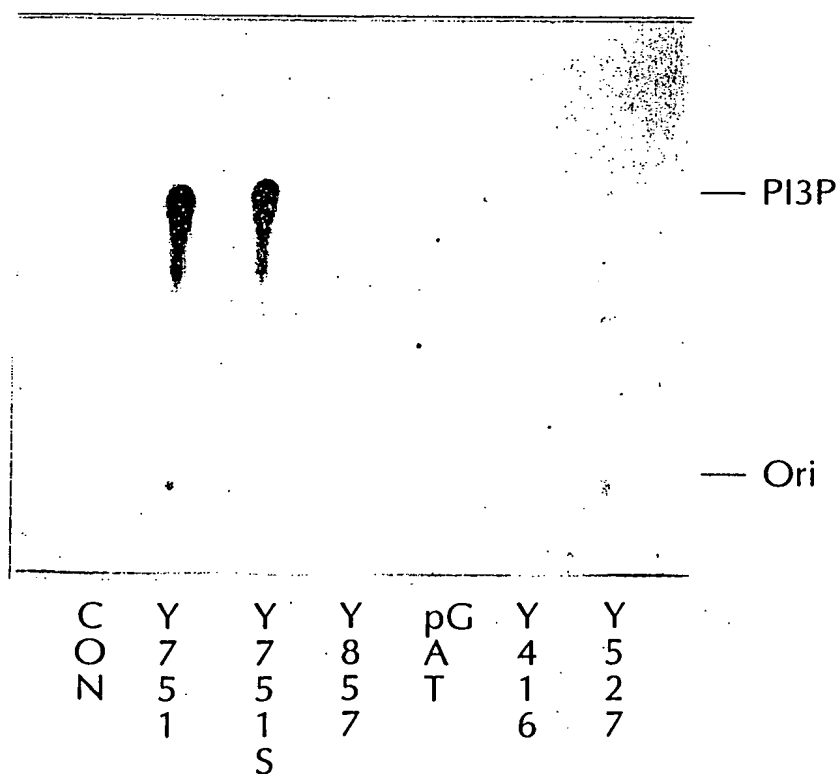


FIG. 8A

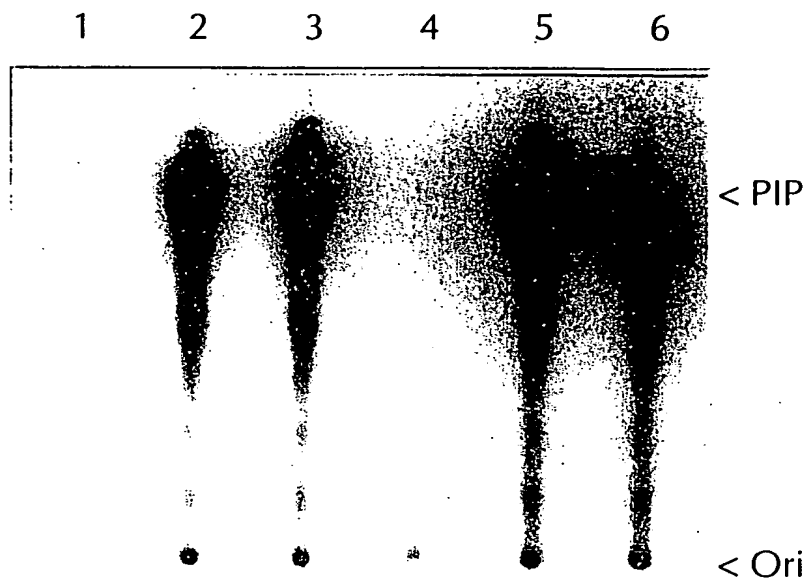


FIG. 8B

751	D M S K D E S V D Y V P M L D M K
751.S	C D E S V D Y V P M L
740	G E S D G G Y M D M S K
1313	E F C P D P L Y E V M L K
Consensus	E E E E E Y M P M X X
	D D D D D V

FIG. 9A

M P P R P S S G E L W G I H L M	16
ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	48
P P R I L V E C L L P N G M I V	32
CCCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGGATGATAGTG	96
T L E C L R E A T L I T I K H E	48
ACTTTAGAAATGCCTCCGTGAGGCTACGTTAATAACGATAAAGCATGAA	144
L F K E A R K Y P L H Q L L Q D	64
CTATTTAAAGAAGCAAGAAAATACCCTCTCCATCAACTTCTTCAAGAT	192
E S S Y I F V S V T Q E A E R E	80
GAATCTTCTTACATTTTCGTAAAGTGTACCCAAGAAGCAGAAAGGGAA	240
E F F D E T R R L C D L R L F Q	96
GAATTTTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTTCAA	288
P F L K V I E P V G N R E E K I	112
CCCTTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATC	336
L N R E I G F A I G M P V C E F	128
CTCAATCGAGAAATTGGTTTTTGCTATCGGCATGCCAGTGTGTGAATTC	384
D M V K D P E V Q D F R R N I L	144
GATATGGTTAAAGATCCAGAAGTACAGGACTTCCGAAGAAATATTCTC	432

FIG. 9B

N V C K E A V D L R D L N S P H 160
AATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT 480
A
S R A M Y V Y P P N V E S S P E 176
AGTAGAGCAATGTATGTTTATCCTCCAAATGTAGAATCTTCACCAGAA 528
L P K H I Y N K L D K G Q I I V 192
CTGCCAAAGCACATATATAATAAATTGGATAAAGGGCAAATAATAGTG 576
V I W V I V S P N N D K Q K Y T 208
GTGATTTGGGTAATAGTTTCTCCAAATAATGACAAACAGAAGTATACT 624
L K I N H D C V P E Q V I A E A 224
CTGAAAATCAACCATGACTGTGTGCCAGAACAAAGTAATTGCTGAAGCA 672
I R K K T R S M L L S S E Q L K 240
ATCAGGAAAAAACTCGAAGTATGTTGCTATCATCTGAACAACTAAAA 720
L C V L E Y Q G K Y I L K V C G 256
CTCTGTGTTTTAGAAATATCAGGGCAAGTATATTTTAAAAGTGTGTGGA 768
C D E Y F L E K Y P L S Q Y K Y 272
TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTAT 816
I R S C I M L G R M P N L M L M 288
ATAAGAAGCTGTATAATGCTTGGGAGGATGCCCAATTTGATGCTGATG 864

FIG. 9C

A K E S L Y S Q L P M D C F T M 304
GCTAAAGAAAGCCTCTATTCTCAACTGCCAATGGACTGTTTACAAATG 912

P S Y S R R I S T A T P Y M N G 320
CCATCATATTCCAGACGCATCTCCACAGCTACGCCATATATGAATGGA 960

^B
E T S T K S L W V I N S A L R I 336
GAAACATCTACAAAATCCCTTTGGGTATATAAATAGTGCACCTCAGAATA 1008

K I L C A T Y V N V N I R D I D 352
AAAATTCTTTGTGCAACCTATGTGAATGTAAATATTCGAGACATTGAC 1056

K I Y V R T G I Y H G G E P L C 368
AAGATTTATGTTTGAACAGGTATCTACCATGGAGGAGAACCCCTTATGT 1104

D N V N T Q R V P C S N P R W N 384
GATAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGAAT 1152

E W L N Y D I Y I P D L P R A A 400
GAATGGCTGAATTACGATATATACATTCCTGATCTTCCTCGTGCTGCT 1200

R L C L S I C S V K G R K G A K 416
CGACTTTGCCTTTCCATTTGTTCTGTTAAAGGCCGAAAGGGTGCTAAA 1248

E E H C P L A W G N I N L F D Y 432
GAGGAACACTGTCCATTGGCCTGGGGAAATATAAACTTGTTTGATTAC 1296

FIG. 9D

T D T L V S G K M A L N L W P V 448
ACAGATACTCTAGTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTA 1344
C
P H G L E D L L N P I G V T G S 464
CCTCATGGACTAGAAAGATTTGCTGAACCCTATTGGTGTACTGGATCA 1392
N P N K E T P C L E L E F D W F 480
AATCCAAATAAAGAAACTCCATGTTTAGAGTTGGAGTTTGACTGGTTC 1440
S S V V K F P D M S V I E E H A 496
AGCAGTGTGGTAAAGTTTCCAGATATGTCAGTGATTGAAGAGCATGCC 1488
N W S V S R E A G F S Y S H A G 512
AATTGGTCTGTATCCCGTGAAGCAGGATTTAGTTATTCCCATGCAGGA 1536
L S N R L A R D N E L R E N D K 528
CTGAGTAACAGACTAGCTAGAGACAATGAATTAAGAGAAAATGATAAA 1584
E Q L R A I C T R D P L S E I T 544
GAACAGCTCCGAGCAATTTGTACACGAGATCCTCTATCTGAAATCACT 1632
E Q E K D F L W S H R H Y C V T 560
GAGCAAGAGAAAGATTTTCTGTGGAGCCACAGACACTATTGTGTAAC 1680
I P E I L P K L L L S V K W N S 576
ATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAAC 1728

FIG. 9E

R D E V A Q M Y C L V K D W P P	592
AGAGATGAAGTAGCTCAGATGTACTGCTTGGTAAAAGATTGGCCTCCA	1776
I K P E Q A M E L L D C N Y P D	608
ATCAAGCCTGAACAGGCTATGGAGCTTCTGGACTGCAATTACCCAGAT	1824
P M V R G F A V R C L E K <u>Y L T</u>	624
CCTATGGTTCGAGGTTTTGCTGTTCGGTGCCTAGAAAAATATTTAACA	1872
<u>D</u>	
D D K L S O Y L I O L V O V L K	640
GATGACAAACTTTCTCAGTACCTAATTCAGCTAGTACAGGTACTAAAA	1920
<u>Y E O Y L D N L</u> L V R F L L K K	656
TATGAACAGTATTTGGATAACCTGCTTGTGAGATTTTACTCAAAAAA	1968
<u>E</u>	
A L T N O R I G H F F F W H L K	672
GCGTTAACTAATCAAAGGATCGGTCACTTTTTCITTTTGCCATTTAAAA	2016
<u>F</u>	
S E M H N K <u>T V S O R F G L L L</u>	688
TCTGAGATGCACAATAAAACAGTTAGTCAGAGGTTTGGCCTGCTTTTG	2064
<u>E S Y C R A C G M Y L</u> K H L N R	704
GAGTCCTATTGCCGTGCATGTGGGATGTATCTGAAGCACCTTAATAGG	2112
<u>G</u>	
Q V E A M E K <u>L I N L T D I L K</u>	720
CAAGTTGAGGCTATGGAAAAGCTCATTAACCTTGACTGACATTCTCAA	2160

FIG. 9F

Q E K K D E T Q K V Q M K F L V	736
CAAGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGT'TTTTAGTT	2208
E Q M R R P D F M D A L Q G F L	752
GAGCAAATGCGGCGACCAGAT'TTCATGGATGCTCTCCAGGGCT'TTCTG	2256
S P L N P A H Q L G N L R L E E	768
TCTCCTCTAAACCTGCTCATCAGCTGGGAAATCTCAGGC'TTGAAGAG	2304
C R I M S S A K R P L W L N W E	784
TGTCGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTGGGAG	2352
N P D I M S E L L F Q N N E I I	800
AACCCAGACATCATGTGAGAATTACTCTTTCAGAACAATGAGATCATC	2400
F K N G D D L R Q D M L T L Q I	816
TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACCCTTCAGATT	2448
I R I M E N I W Q N Q G L D L R	832
ATTCGCATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGA	2496
M L P Y G C L S I G D C V G L I	848
ATGTTACCTTATGGATGTCTGTCAATCGGTGACTGTGTGGGACTTATC	2544
E V V R N S H T I M Q I Q C K G	864
GAGGTGGTGAGAAATTCTCACACTATAATGCAGATTCAGTGTAAGGA	2592

FIG. 9G

H
G L K G A L O F N S H T L H Q W 880
GGCCTGAAAGGTGCACTGCAGTTTAACAGCCACACTCCATCAGTGG 2640

L K D K N K G E I Y D A A I D L 896
CTCAAAGACAAGAACAAGGGGGAATATATGATGCGGCCATCGATTTG 2688

I
F T R S C A G Y C V A T F I L G 912
TTTACACGATCATGTGCTGGATATTGTGTTGCCACCTTCATTTTGGGA 2736

I G D R H N S N I M V K D D G O 928
ATTGGAGATCGTCACAATAGTAATATCATGGTTAAAGATGATGGACAA 2784

J
L F H I D F G H F L D H K K K K 944
CTGTTTCATATAGATTTTGGACACTTTTGGGATCACAAGAAGAAAAA 2832

K
F G Y K R E R V P F V L T O D F 960
TTTGGTTATAAACGAGAGCGCGTGCCGTTTGTTTTGACACAAGATTTTC 2880

L I V I S K G A Q E C T K T R E 976
TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA 2928

F E R F Q E M C Y K A Y L A I R 992
TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGG 2976

		<i>L</i>																
<u>O</u>	<u>H</u>	<u>A</u>	<u>N</u>	<u>L</u>	<u>F</u>	<u>I</u>	<u>N</u>	<u>L</u>	<u>F</u>	<u>S</u>	<u>M</u>	<u>M</u>	<u>L</u>	<u>G</u>	<u>S</u>	1008		
CAGCATGCCAATCTCTTCATAAATCTTTCTCAATGATGCTTGGCTCT																3024		
<u>G</u>	<u>M</u>	<u>P</u>	<u>E</u>	<u>L</u>	<u>Q</u>	<u>S</u>	<u>F</u>	<u>D</u>	<u>D</u>	<u>I</u>	<u>A</u>	<u>Y</u>	<u>I</u>	<u>R</u>	<u>K</u>	1024		
GGAATGCCAGAACTGCAATCTTTTGATGATATTGCATACATTGAAAG																3072		
<i>M</i>																		
<u>T</u>	<u>L</u>	<u>A</u>	<u>L</u>	<u>D</u>	<u>K</u>	<u>T</u>	<u>E</u>	<u>O</u>	<u>E</u>	<u>A</u>	<u>L</u>	<u>E</u>	<u>Y</u>	<u>F</u>	<u>M</u>	1040		
ACCCTAGCTTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTTCATG																3120		
<u>K</u>	<u>Q</u>	<u>M</u>	<u>N</u>	<u>D</u>	<u>A</u>	<u>H</u>	<u>H</u>	<u>G</u>	<u>G</u>	<u>W</u>	<u>T</u>	<u>T</u>	<u>K</u>	<u>M</u>	<u>D</u>	1056		
AAACAAATGAATGATGCACACCATGGTGGCTGGACAACAAAATGGAT																3168		
<i>N</i>																		
<u>W</u>	<u>I</u>	<u>F</u>	<u>H</u>	<u>T</u>	<u>I</u>	<u>K</u>	<u>Q</u>	<u>H</u>	<u>A</u>	<u>L</u>	<u>N</u>	<u>*</u>	1069					
TGGATCTTCCACACAATTAAGCAGCATGCTTTGAACTGA												3207						

+

FIG. 9I

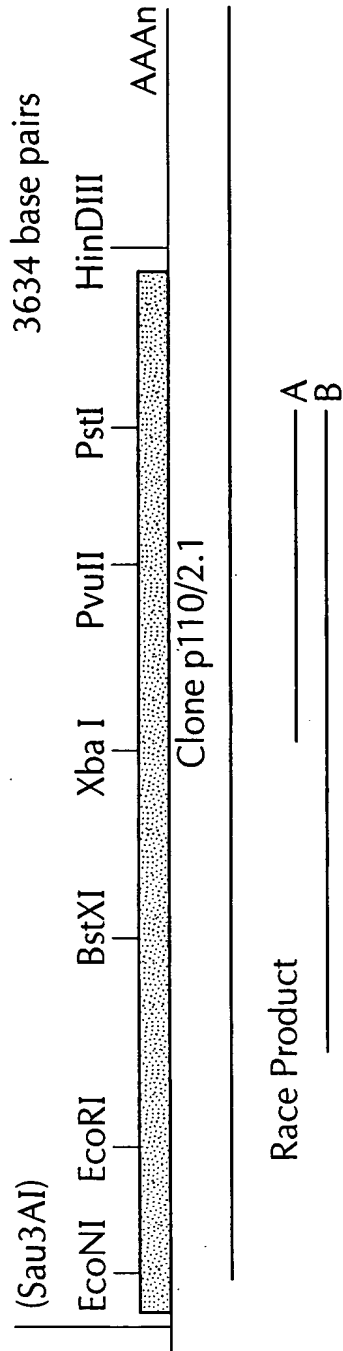


FIG. 10A

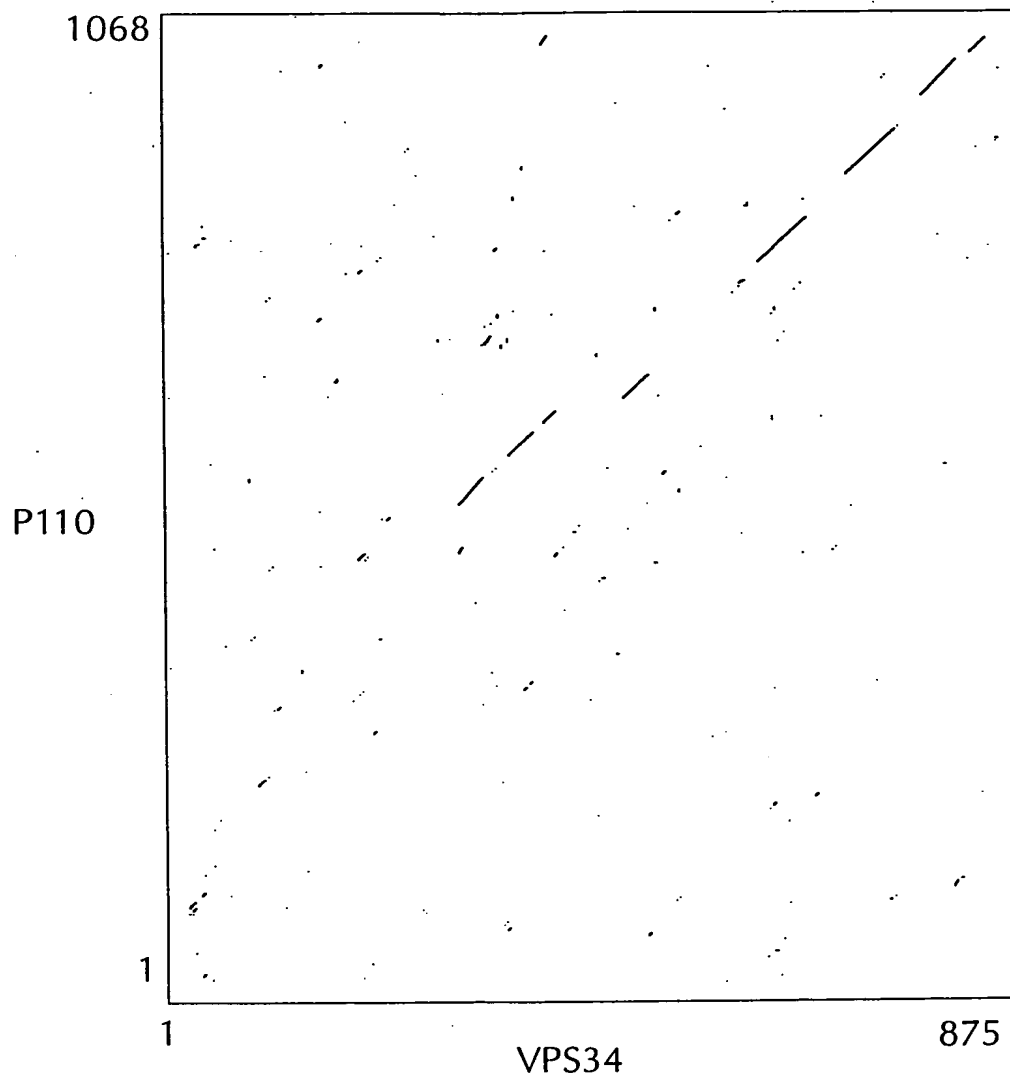


FIG. 10B

P110 VCEFDMVKDPEVQDFRRNILNVCKEAVDLRLNSPHSRAMYVYPPN 170
..| : .| :|. :: .| .: . : |:. .. .:: :...|
VPS34 NITFCVSQDLDVP.LKVKIKSLEGHKPLLKPSQKIILNPEIMLIGSN 49
171 VESSPEL..PKHIYNKLDKGQIIIVVIWVIVSPNNDKQKYTLKINHDCVPE 218
|.|.:.| . :::|. . :::|. :|. | ::::.....
50 VFPSSDLIVSLQVFDKERNRNLTLPIYTPYIPFRNSRTWDYWL..... 92
219 QVIAEAIRKKTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYFLEKYPLS 268
... ::: : :|| :|:::|:|.|
93TLPIRIKQLTFSS.HLRILWEYNG..... 116
269 QYKYIRSCIMLGRMPNLMIMAKESLYSQLPMDCE*TMP*SYSRRISTATPYM 318
|...|::
117SKQIPFF 123
319 NGETSTKSLWVINSALRIKILCATYVNVNIRDIDKIYVRTGIYHGGEPLC 368
| |||. : : :. :| :|::: .| :... .|.:
124 NLETSI..FNLKDCTLK.....RGFESLKFRYDVIDHCEVVT 158
369 DNVNTQRVPCSNPRWNEWLN*YDIYIPDL*PRAARLC.LSICSVKGRKGAKE 417
|| : .| || ... :. :| :. :|::: ::::
159 DNKD.....QENLN.KYFQGEF*TRLPWLDEITISKLRKQRENRT 196

FIG. 10C

418 .EHCPLAWG.NINLFDYTDTLVSGKMAINLWVPVPHGLEDLLNPIGVTGS. 464
..... :: :.... ::. : . : | . | | | :...
197 WPQGTFVLNLEFPMLELPVVFIEREIMNTQMNIP....TLKNNPGLSTD 242
465 .NPNKETPCLELEF.DWFSSVVKFPDMSVIEEHANWSVSREAGFSYSHAG 512
:|:|:| : : : : | : : | : | : : : | .. | : : : | :
243 REPNRNDPQIKISLGDKYHSTLKFYD....PDQPNNDPIEEKYRRLERAS 288
513 LSNRLARDNELRENDKEQLRAICTRDPLSEITEQEKFDFLWSHRHYCVTIP 562
...|: : : : : : : | . | . . | : : | : | : : | : | : | : .
289 KNANLDKQVKPDIKKRDYLNKIINYPGGTKLTAHEKGSIWKYRYIIMNNK 338
563 EILPKLLLSVKWNSRDEVAQMYCLVKDWPPIKPEQAMELIDCNPDPMPVR 612
. | . | | | | : : : . . | : : : | : : | : : | : : | : : : : | |
339 KALTKLLQSTNLREESERVEVLELMDSWAEIDIDDALELLGSTFKNLSVR 388
613 GFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQY..... 644
: : | | . | . | . | . | . | : : | : | : : : : | : .
389 SYAVNRLKK.ASDKELELYLLQLVEAVCFENLSTFSDKSNSEFTTIVDAVS 437
645LDNLLVRFLLKK 656
: . | . | : : :
438 SQKLSGDSMLLSTSHANQKLLKSISSESETSGTESLPIVISPLAEFLIRR 487

FIG. 10D

657 ALTNQRIGHFFFWHLKSEMHNKTVSQRFGLLLESY.CRACGMYLKHLNRQ 705
| | . | . | : | | | : | . | | | | . : | . : : | . | : : | . . | | |
488 ALVNPRLGSSFFYWYLKSESEDKPY...LDQILSSFWRLDKKSRNINLNDQ 534
706 VEAMEKLINLTDILKQEKKDETQKVQMKF.LVEQMRRPDMDALQGFLSP 754
| : : | : : : | . | | : : . | : | . | | : : : : |
535 VRLINVLRECCETIKRLKDTTAKKMELLVHLLLETQVRP..LVKVRPIALP 582
755 LNPAHQLGNLRLLEECRIMSSAKRPLWLNWENPDIMSELLFQNNELIFKNG 804
| : | . : : : | . : : : : | . | | : : : : | | : : : | |
583 LDPDVLICDVCPETSKVFKSSLSPLKITFKTT.....LNQPYHLMFKVG 626
*
805 DDLRQDMLTLQIIRIMENTIWQNOGLDLRLMPYGCLSIGDCVGLIEVVRNS 854
| | | | | | . : | | | . : : : : | . : : : | | . | . | . | | : : . |
627 DDLRQDQLVVQIISLMNELLKNENVDLKLTPYKILATGPQEGAEFIPN. 675
*
855 HTIMQIQCK.GGLKGALQFNSHTLHQWLKDKNKGEIYDAAIDLFTRSCAG 903
| : | : | | : | | : : : : : : : : : : | | : | | | |
676 DTLASILSKYHGILGYLKL.....HYPDENATLGVGQWLDNFVKSCAG 719
* * *
904 YCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKKKFGYKRERVP 953
| | | | : | | | : | | | . | : : | . | | : | | | | | | : | : : . | . |
720 YCVITYILGVGDRHLDNLLVTPDGHFFHADFGYILGQDPKPF.....P 762
954 FVLTDQFLIVISKGAQECTKTREFERFQEMCYKAYLAIROHANLFINLFS 1003
: : . . | : . | : | : . : : : | . | : | | : | : | . | : : | | | .
763 PIMKLPPQIIEAFGGAESS...NYDKFRSYCFVAYSILRRNAGLIILNLFE 809
1004 MMLGSGMPE..LQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGW 1051
: | . | : | : : : . : | : | . : . | : : | : | . | : | | . : : :
810 IMKTSNIPDIRIDPNGAILRVRERFNLNMSEEDATVHFQNLINDSVNALL 859
1052 TTKMDWIFHTIKQH 1065
.. : | : | : | .
860 PIVIDH.LHNLAQY 872

FIG. 11B

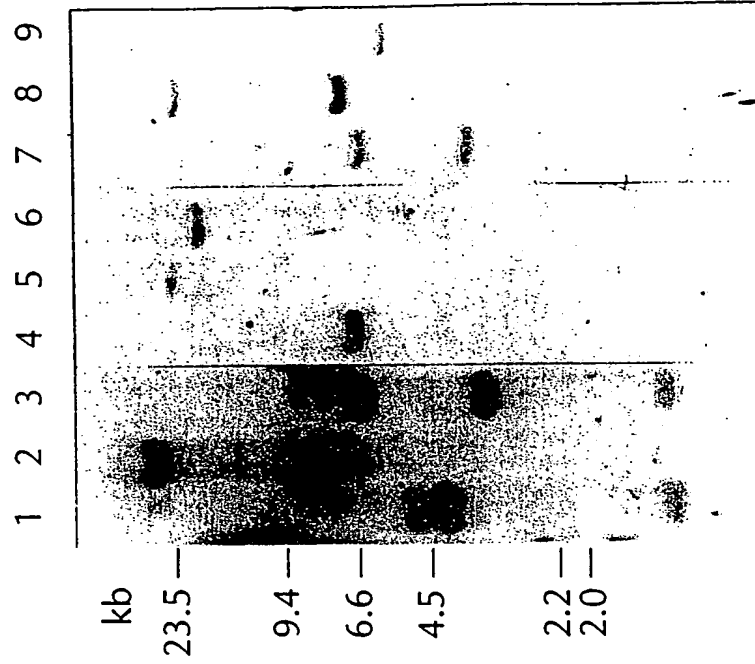


FIG. 11A

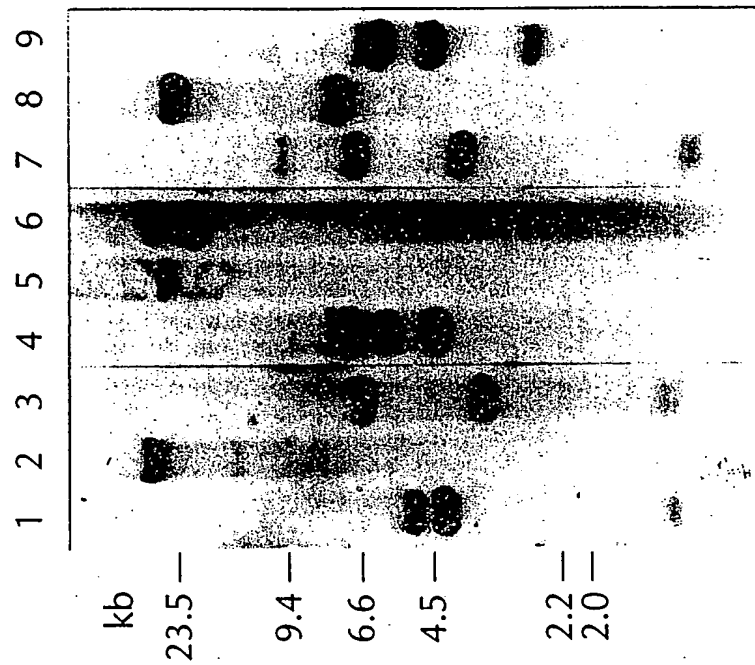


FIG. 12A

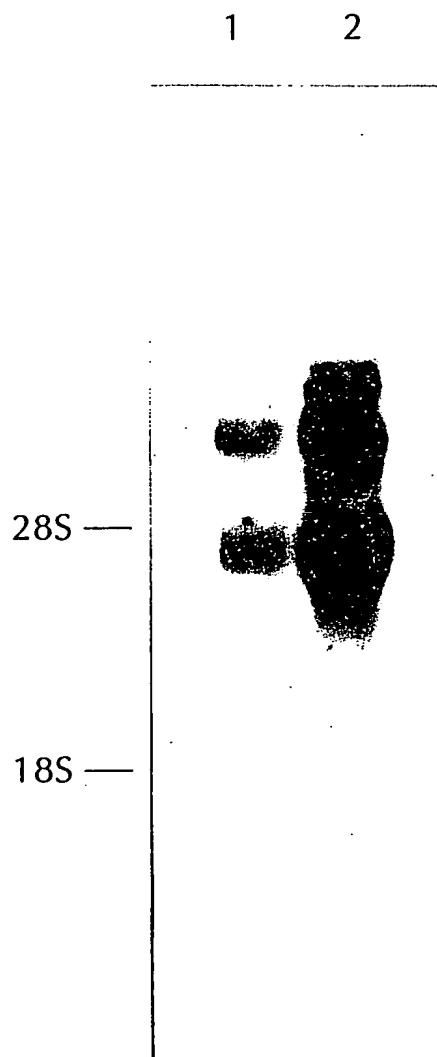


FIG. 12B

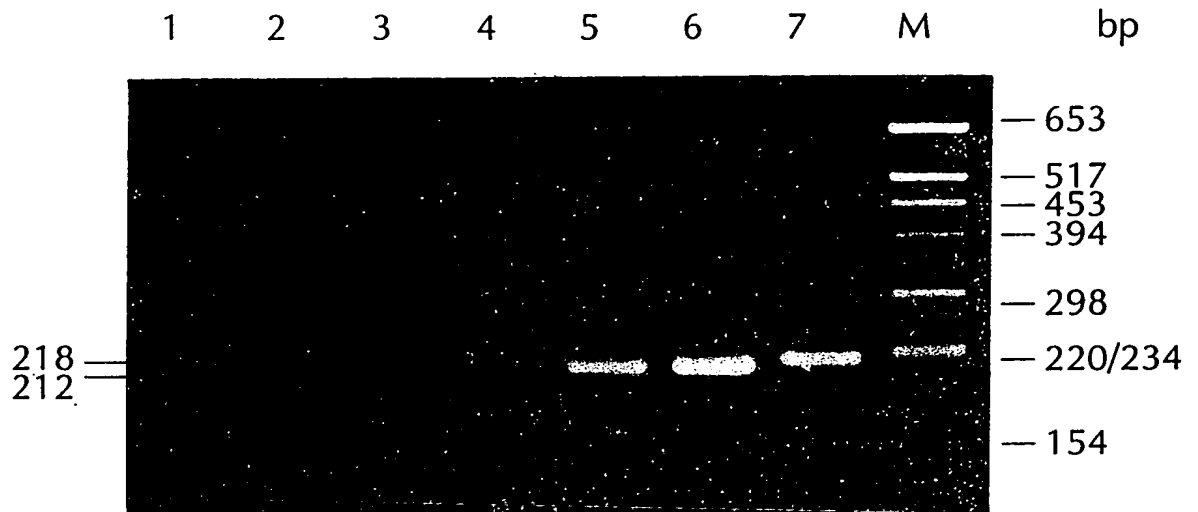


FIG. 12C

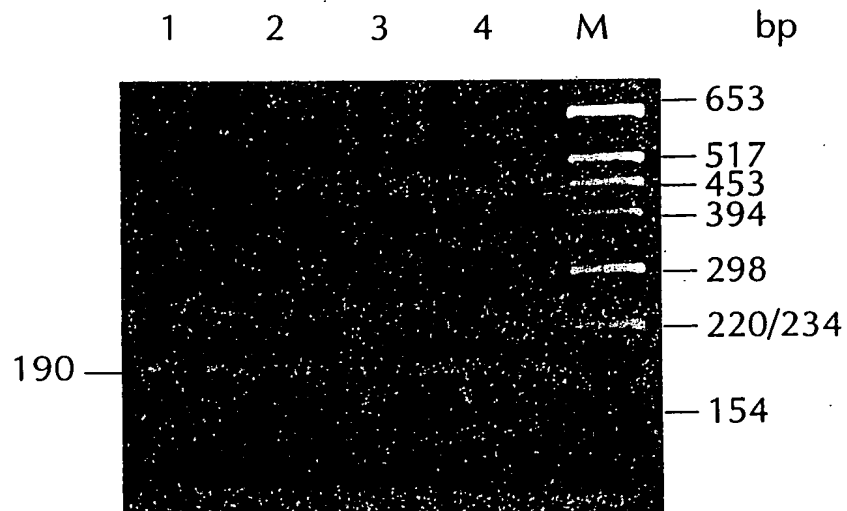


FIG. 13A

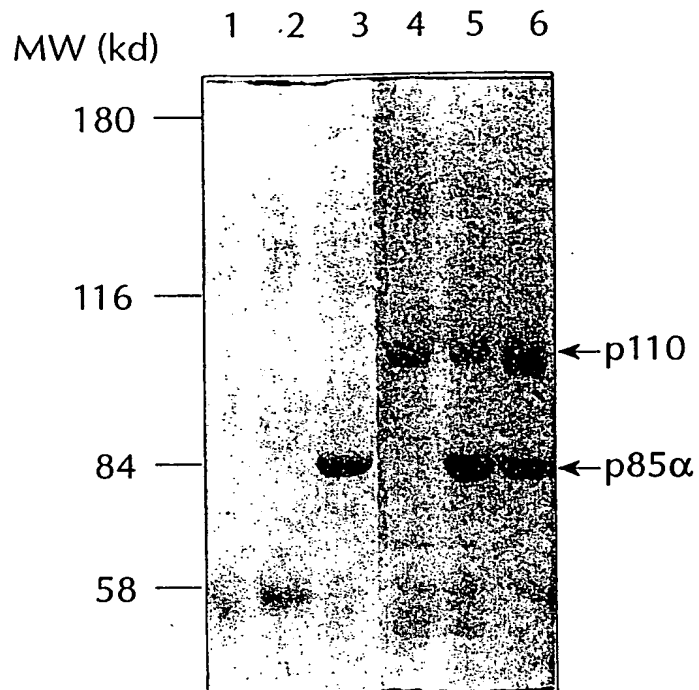


FIG. 13B

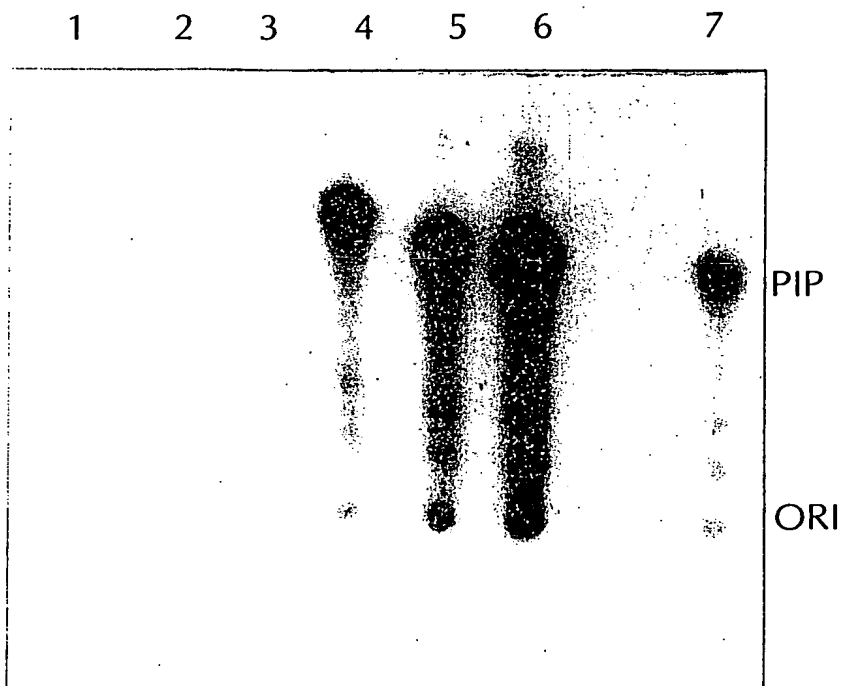


FIG. 14A

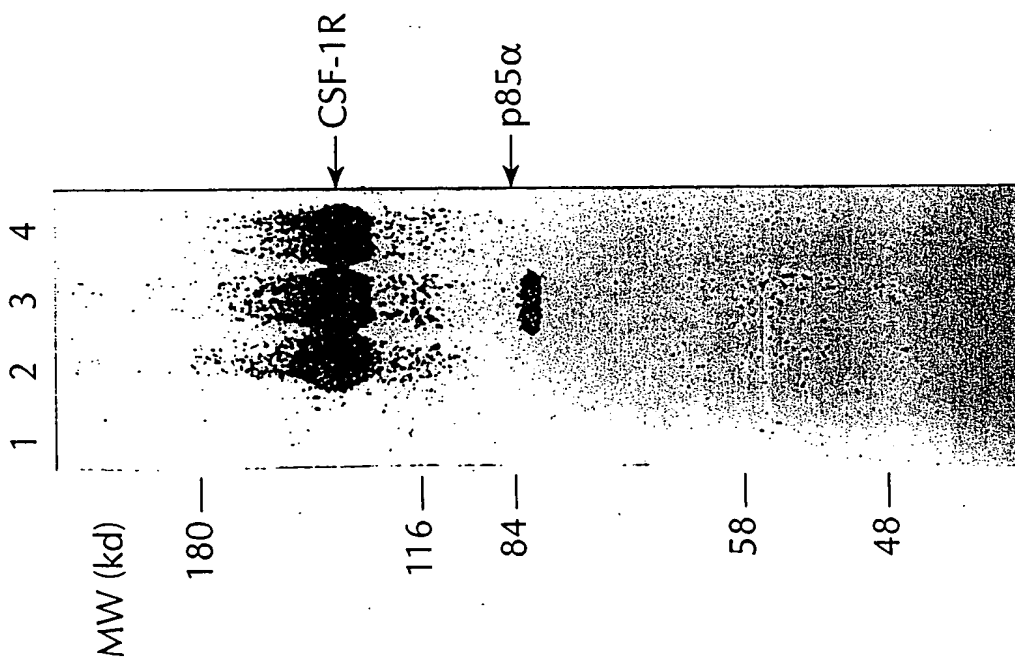


FIG. 14B

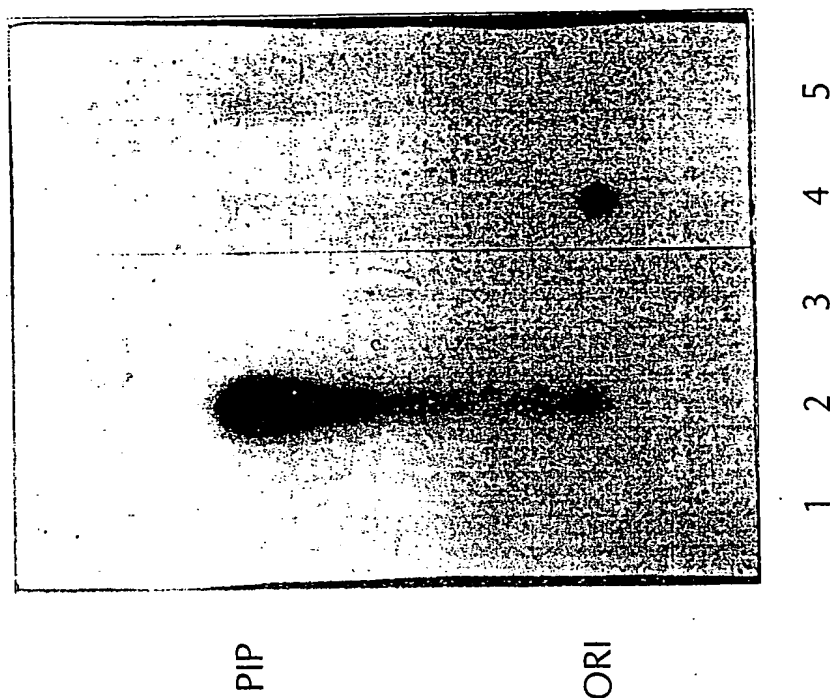


FIG. 15A

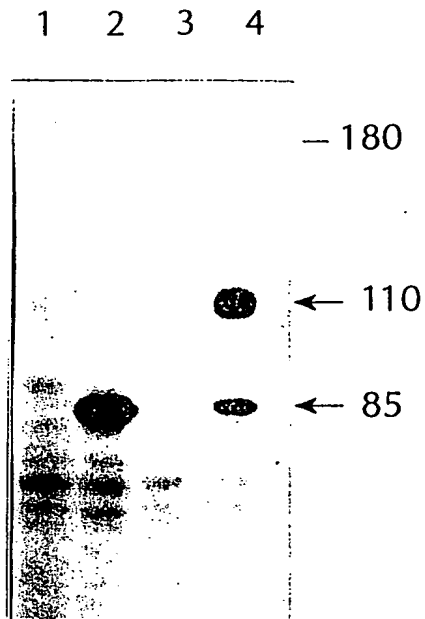


FIG. 15B

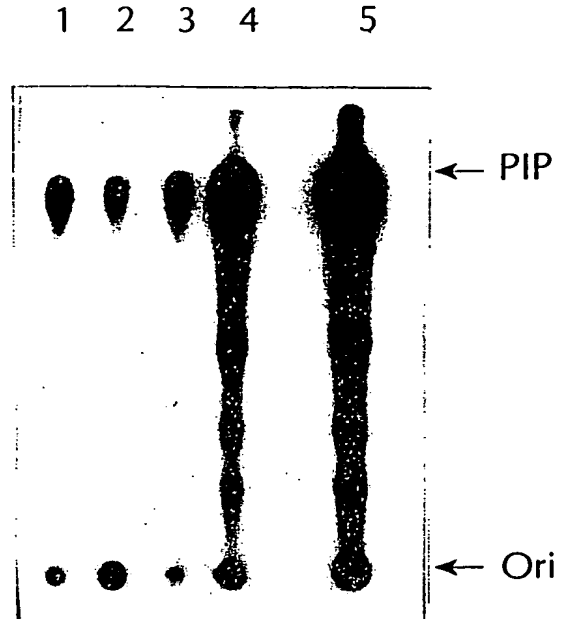


FIG. 15C

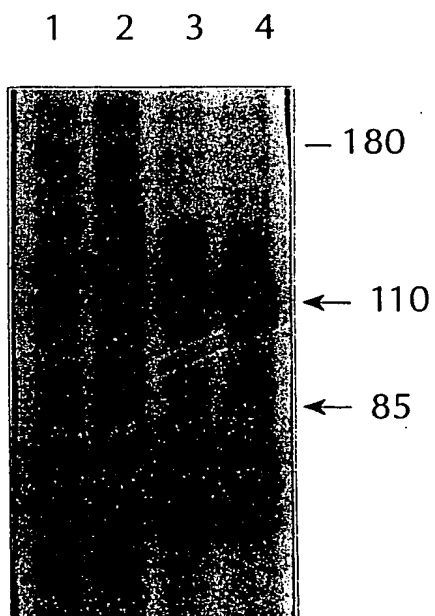


FIG. 15D

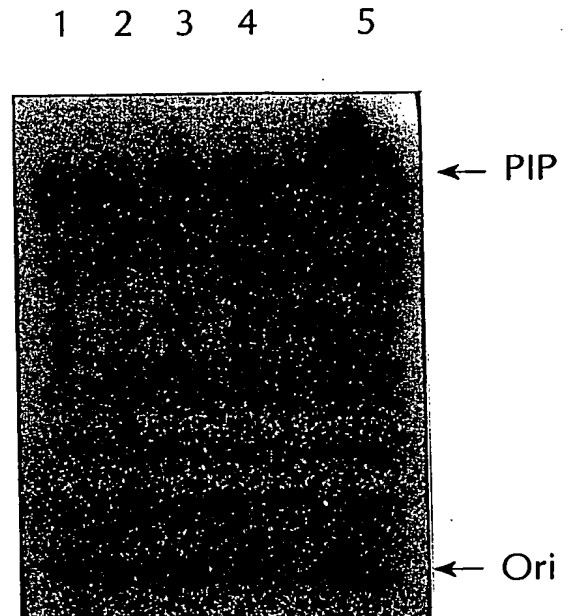


FIG. 16A

```
1      ATGCCTCCAAGACCATCATCAGGTGAACCTGTGGGCATCCACTTGATG      48
      -----+-----+-----+-----+-----+-----+-----
      TACGGAGGTTCTGGTAGTAGTCCACTTGACACCCCGTAGGTGAACCTAC
      M P P R P S S G E L W G I H L M

49      CCCCCAAGAAATCCTAGTGGAAATGTTTACTACCAAAATGAATGATAGTG      96
      -----+-----+-----+-----+-----+-----+-----
      GGGGTTCTTAGGATCACCTTACAAATGATGGTTTACCTTACTATCAC
      P P R I L V E C L L P N G M I V

97      ACTTTAGAAATGCCCTCCGTGAGGCTACATTAGTAACATAAAGCATGAA      144
      -----+-----+-----+-----+-----+-----+-----
      TGAAATCTTACGGAGGCACTCCGATGTAATCATTCATGATATTTCGTACTT
      T L E C L R E A T L V T I K H E

145     CTATTTAAAGCAAGCAAGAAATACCCCTCTCCATCAACTTCTTCAAGAT      192
      -----+-----+-----+-----+-----+-----+-----
      GATAAATTCTTCGTTCTTTTATGGAGAGGTAGTTGAAGAAGTTCTA
      L F K E A R K Y P L H Q L L Q D
```

FIG. 16B

193 GAATCTTCTTACATTTTCGTAAGTGTTACCCAAAGACAGAAAGGAA
-----+-----+-----+-----+-----+
CTTAGAAGAAATGTAAAAGCATTCAACAATGGGTTCTTCGTCCTTCCCTT
E S Y I F V S V T Q E A E R E 240

241 GAATTTTGTGATGAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA
-----+-----+-----+-----+-----+
CTTAAAAAACTACTTTGTCTGCTGAAACACTAGAACCCGAAAGTT
E F F D E T R R L C D L R L F Q 288

289 CCATTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAAGAAAGATC
-----+-----+-----+-----+-----+
GGTAAAAATTTTCATTAACTTGGTCATCCGTTGGCCTTCTTTCTAG
P F L K V I E P V G N R E E K I 336

337 CTCATCGAGAAATTGGTTTTCGTATCGGCATGCCAGTGTCGGAATTT
-----+-----+-----+-----+-----+
GAGTTAGCTCTTTAACCAAAACGATAGCCGTACGGTACACGCTTAA
L N R E I G F A I G M P V C E F 384

FIG. 16C

385 GATAATGGTTAAAGATCCTGAAGTACAGGACTTCCGAAGAAATATTCCTT
-----+-----+-----+-----+-----+-----+-----+
CTATACCAATTCTTAGGACTTCATGTCCTGAAGGCTTCTTTATAAGAA
D M V K D P E V Q D F R R N I L
432

433 AATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT
-----+-----+-----+-----+-----+-----+-----+
TTACAAACATTTCTTCGACACCTAGAATCCCTAGAATTAAGTGGAGTA
N V C K E A V D L R D L N S P H
480

481 AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAAATCTTCACCAGAG
-----+-----+-----+-----+-----+-----+-----+
TCATCTCGTTACATACAGATAGCGGGTGTAATCTTAGAAGTGGTCTC
S R A M Y V Y P P H V E S S P E
528

529 CTGCCAAAGCACATATATAATAAATGGATAGAGGCCAAATAATAGTG
-----+-----+-----+-----+-----+-----+-----+
GACGGTTTCGTATATATTTAACCCTATCTCCGGTTTATATCAC
L P K H I Y N K L D R G Q I I V
576

FIG. 16D

577 GTGATTTGGGTAATAGTTTCTCCAAATAATGACAAGCAGAAAGTATACT
-----+-----+-----+-----+-----+-----
CACTAAACCCATTATCAAGAGGTTTATTACTGTTCGTCTTCATATGA
V I W V I V S P N N D K Q K Y T
624

625 CTGAAAATCAACCATGACTGTGTGCCAGAACAAAGTAATTGCTGAAGCA
-----+-----+-----+-----+-----+-----
GACTTTTAGTTGGTACTGACACACGCGTCTTGTTCATTAAACGACTTCGT
L K I N H D C V P E Q V I A E A
672

673 ATCAGGAAAAAAGTAAAGTATGTGTGCTATCATCTGAACAATTAAAA
-----+-----+-----+-----+-----+-----
TAGTCCCTTTTGTGATCTTCATACACGATAGTAGACTTGTTAATTTT
I R K K T R S M L L S S E Q L K
720

721 CTCGTGTTTAGAATATCAGGGCAAGTACATTTTAAAAAGTGTGTGGA
-----+-----+-----+-----+-----+-----
GAGACACAAAATCTTATAGTCCCGTTCATGTAAATAATTTTCACACACCT
L C V L E Y Q G K Y I L K V C G
768

FIG. 16E

```
769      TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTAT      816
      -+-----+-----+-----+-----+-----+-----+
      A C A C T A C T T A T G A A G G A T C T T T T A T A G G A C T C A G T C A T A T T C A T A
      C D E Y F L E K Y P L S Q Y K Y
817      A T A A G A A G C T G T A T A A T G C T T G G G A G A T G C C C A A T T T G A A G A T G A T G
      ---+-----+-----+-----+-----+-----+-----+
      T A T T C T C G A C A T A T T A C G A A C C C T C C T A C G G G T T A A A C T T C T A C T A C
      I R S C I M L G R M P N L K M M
865      G C T A A A G A A G C C T T T A T T C T C A A C T G C C C A A T G G A C T G T T T A C A A T G
      ---+-----+-----+-----+-----+-----+-----+
      C G A T T T C T T T C G G A A A T A A G A G T T G A C G G T T A C C T G A C A A A A T G T T A C
      A K E S L Y S Q L P M D C F T M
913      C C A T C T T A T T C C A G A C G C A T T T C C A C A G C T A C C A T A T A T G A A T G G A
      ---+-----+-----+-----+-----+-----+-----+
      G G T A G A A T A A G G T C T G C G T A A A G G T G T C G A T G T G G T A T A T A C T T A C C T
      P S Y S R R I S T A T P Y M N G      960
```

FIG. 16F

```

961      GAAACATCTACAAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA
      1008
      CTTGTAGATGTTTAGGAAACCCAAATATTATCTCGTGAGTCTTAT
      E T S T K S L W V I N R A L R I
      1056
      AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGAC
      TTTTAAGAAACACGTTGGATGCACTTAGATTATTAAGCTCTGTAACTG
      K I L C A T Y V N L N I R D I D
      1104
      AAGATTATGTTCGAACAGGTATCTACCATGGAGGAGAACCCCTTATGT
      TTCTAAATACAAGCTTGTCATAGATGGTACCTCCTCTTGGGAATACA
      K I Y V R T G I Y H G G E P L C
      1152
      GACAAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGAAT
      CTGTTACACTTGTGAGTTTCTCATGGAACAAGTTAGGGTCCACCTTA
      D N V N T Q R V P C S N P R W N

```

+

[illegible]

FIG. 16H

```
1345 CCTCATGGATTAGAAGATTGCTGAACCCCTATTGGTGTACTGGATCA
      +-----+-----+-----+-----+-----+-----+
      GGAGTACCTAATCTTCTAAACGACTTGGGATAACCAACAATGACCTAGT
      P H G L E D L L N P I G V T G S
1392
      AATCCAAATAAGAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC
      +-----+-----+-----+-----+-----+-----+
      TTAGGTTTATTTCTTGAGGTACGAATCTCAACCTCAAACTGACCAAG
      N P N K E T P C L E L E F D W F
1440
      AGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC
      +-----+-----+-----+-----+-----+-----+
      TCGTCACACCATTTCAAGGGTCTATACAGTCACCTAATCTCTCGTACGG
      S S V V K F P D M S V I E E H A
1488
      AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGA
      +-----+-----+-----+-----+-----+-----+
      TTAACCGACATAGGGCTCTTCGTCCTAAATCGATAAGGTGCGTCCT
      N W S V S R E A G F S Y S H A G
1536
```

FIG. 16I

```
1537 CTGAGTAAACAGACTAGCTAGACACAATGAATTAAGGAAAATGACAAA  
-----+-----+-----+-----+-----+-----  
GACTCAATTGCTGATCGATCTCTGTACTTAATTCCTTTTACTGTTT  
L S N R L A R D N E L R E N D K  
1584  
1585 GAACAGCTCAAAGCAATTCTACACGAGATCCTCTCTCTGAAATCACT  
-----+-----+-----+-----+-----+-----  
CTTGTCGAGTTTCGTTAAAGATGTGCTCTAGGAGAGAGACTTTAGTGA  
E Q L K A I S T R D P L S E I T  
1632  
1633 GAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAAC  
-----+-----+-----+-----+-----+-----  
CTCGTCCTCTTTTCTAAAGATACCTCAGTGTCTGTGATAACACATTGA  
E Q E K D F L W S H R H Y C V T  
1680  
1681 ATCCCCGAAATTCTACCCCAAATTGCTTCTGTCTGTAAATGGAATTCT  
-----+-----+-----+-----+-----+-----  
TAGGGGCTTTAAGATGGGTTTAAACGAAGACAGACAAATTACCTTAAGA  
I P E I L P K L L L S V K W N S  
1728
```

FIG. 16J

1729	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAGATTGGCCTCCA +-----+-----+-----+-----+-----+-----+ TCTTACTTCATCGGGTCTACATAACGAACCATTTTCTAACCGGAGGT R D E V A Q M Y C L V K D W P P	1776
1777	ATCAAACCTGAACAGGCTATGGAACCTTCTGGACTGTAATTACCCAGAT - - - - - + - - - - - + - - - - - + - - - - - + - - - - - TAGTTTGGACTTGTCCGATACCTTGAAGACCTGACATTAATGGGTCTA I K P E Q A M E L L D C N Y P D	1824
1825	CCTATGGTTCGAGGTTTGTCTGTTCTGGTCTTGGAAAAATATTAAACA - - - - - + - - - - - + - - - - - + - - - - - + - - - - - GGATACCAAGCTCCAAAACGACAAGCCACGAACCTTTTATATAAATTGT P M V R G F A V R C L E K Y L T	1872
1873	GATGACAAACTTCTCAGTATTTAAATTCAGCTAGTACAGGTCCATAAA - - - - - + - - - - - + - - - - - + - - - - - + - - - - - CTACTGTTTGAAAGAGTCATAAAATTAAGTCGATCATGTCCAGGATTT D D K L S Q Y L I Q L V Q V L K	1920

FIG. 16K

1921 TATGAACAATATTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA
-----+-----+-----+-----+-----
1968 ATACTTGTATAAACCTATTGAACGAACACTCTAAAAATGACTTCTTT
Y E Q Y L D N L L V R F L L K K
2016 GCATTGACTAATCAAGGATTGGGCACTTTCTTTTGGCATTAAAA
-+-----+-----+-----+-----+-----
CGTAACGATGATTTCCTAACCCGTGAAAAAGAAACCGTAAATTTT
A L T N Q R I G H F F F W H L K
2064 TCTGAGATGCACAATAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTG
-----+-----+-----+-----+-----
AGACTCTACGTGTTATTTTGTCAATCGGTCTCCAAACCGGACGAAAC
S E M H N K T V S Q R F G L L L
2112 GAGTCCCTATTGTCGTGCATGTGGGATGTTTGAAGCACCTGAATAGG
-----+-----+-----+-----+-----
2065 CTCAGGATAACAGCACGTACACCCCTACATAAACTTCGTGGACTTATCC
E S Y C R A C G M Y L K H L N R

FIG. 16L

```
2113      CAAAGTCGAGGCAATGGAAAAGCTCATTAACCTAAGTACATCTCTCAAA
      +-----+-----+-----+-----+-----+-----+
      GTTCAGCTCCGTTACCTTTTCGAGTAATTGAATTGACTGTAAGAGTTT
      Q V E A M E K L I N L T D I L K

2161      CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTAGTT
      +-----+-----+-----+-----+-----+-----+
      GTCCTCTCCTTCCTACTTTTGTTGTTTTCCTATGTCCTACTTCAAAAATCAA
      Q E R K D E T Q K V Q M K F L V

2209      GAGCAAAATGAGCGGACCAGATTTCATGGATGCCCTACAGGGCTTGCTG
      +-----+-----+-----+-----+-----+-----+
      CTCGTTTACTCCGCTGGTCTAAAGTACCTACGGGATGTCCTCCGAACGAC
      E Q M R R P D F M D A L Q G L L

2257      TCTCCTCTAAACCCCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAG
      +-----+-----+-----+-----+-----+-----+
      AGAGGAGATTTGGACGAGTAGTTGATCCTTTGGAGTCCGAATTCTC
      S P L N P A H Q Q L G N L R L K E
```

2160

2208

2256

2304

$+$

2305	TGTCGAATTATGTCTTCTGCAAAAAGGCCCACTGTGGTTGAATTGGGAG -----+-----+-----+-----+-----+-----+-----+ ACAGCTTAATACAGAAGACGTTTTTCCGGTGACACCAACTTAACCCCTC C R I M S S A K R P L W L N W E	2352
2353	AACCCAGACATCATGTCAGAGTTACTGTTCAGAAACAATGAGATCATC -----+-----+-----+-----+-----+-----+-----+ TTGGGCTCTGTAGTACAGTCTCAATGACAAAGTCTTGTTACTCTAGTAG N P D I M S E L L F Q N N E I I	2400
2401	TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATT -----+-----+-----+-----+-----+-----+-----+ AAATTTTACCCCTACTAAATGCCGTTCTATACGATTGTGAAGTTTAA F K N G D D L R Q D M L T L Q I	2448
2449	ATTCGTATTATGGAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGA -----+-----+-----+-----+-----+-----+-----+ TAAGCATAATACCTTTTATAGACCGTTTGTAGTCCAGAACTAGAAGCT I R I M E N I W Q N Q G L D L R	2496

FIG. 16N

```
2497 ATGTTACCTTATGGTGTCTGTCAATCGGTGACTGTGTGGGACTTATT  
2544 -----+-----+-----+-----+-----+-----  
TACAATGGAATACCAACAGACAGTTAGCCACTGACACACCCCTGAATAA  
M L P Y G C L S I G D C V G L I  
2592 GAGGTGGTGCGAATTCACACTATTATGCAAAATTCAGTGCAAAAGGC  
2593 -----+-----+-----+-----+-----+-----  
CTCCACCCACGCTTTAAGAGGTGATAATACGTTTAAGTCACGTTTCCG  
E V V R N S H T I M Q I Q C K G  
2593 GGCTTGAAAGGTGCACCTGCAGTTCACAGCCACACACTACATCAGTGG  
2593 -----+-----+-----+-----+-----+-----  
CCGAACTTCCACGTGACGTCAGTTGTCGGTGTGTGATGTAGTCACC  
G L K G A L Q F N S H T L H Q W  
2641 CTCAAAGACAAGAAACAAGGAGAAATATATGATGCAGCCATTGACCTG  
2688 -----+-----+-----+-----+-----+-----  
GAGTTTCTGTTCTTTCCTCTTTATATACGTACGTCGGTAACCTGGAC  
L K D K N K G E I Y D A A I D L
```

FIG. 160

2689 TTTACACGTTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGA
-+-----+-----+-----+-----+-----+-----+
AAATGTGCAAGTACACGACCTATGACACATCGATGGAAGTAAACCCCT
F T R S C A G Y C V A T F I L G
2736
2737 ATTGGAGATCGTCACAAATAGTAACATCATGGTGAAAGACGATGGACAA
---+-----+-----+-----+-----+-----+-----+
TAACCTCTAGCAGTGTATCATGTGTAGTACCACCTTTCTGTACCTGTT
I G D R H N S N I M V K D D G Q
2784
2785 CTGTTTCATATAGATTTTGGACACTTTTGGATCACAAGAAGAAAAAA
-----+-----+-----+-----+-----+-----+
GACAAAGTATATCTAAACCTGTGAAAAACCTAGTGTCTTCTTTT
L F H I D F G H F L D H K K K K
2832
2833 TTTGGTTATAAACGAGAACGTGTGCCATTGTTTGGACACAGGATTTC
-----+-----+-----+-----+-----+-----+
AAACCAATATTTGCTCTTGCACACGCGTAACAAAACTGTGTCTTAAG
F G Y K R E R V P F V L T Q D F
2880

FIG. 16P

```
2881 TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA
-----+-----+-----+-----+-----+-----+
AATTATCACTAATTCCTCGGTTCTTACGTGTTTCTGTTCTCTTT
L I V I S K G A Q E C T K T R E

2929 TTTGAGAGGTTTCAGGAGATGTGTACAAAGGCTTATCTAGCTATTCTGA
-+-----+-----+-----+-----+-----+-----+
AAACTCTCCAAAGTCCCTACACAAATGTTCCGAATAGATCGATAAGCT
F E R F Q E M C Y K A Y L A I R

2977 CAGCATGCCAATCTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCT
-+-----+-----+-----+-----+-----+-----+
GTCGTACGGTTAGAGAAGTATTTAGAAAAGAGTTACTACGAACCGAGA
Q H A N L F I N L F S M M L G S

3025 GGAATGCCAGAACTACAATCTTTTGATGACATTGCATACATTCGAAAG
-+-----+-----+-----+-----+-----+-----+
CCTTACGGTCTTGATGTTAGAAAACACTACTGTAACTGATGTAGCTTTC
G M P E L Q S F D D I A Y I R K

2928
2976
3024
3072
```

FIG. 16Q

3073	ACCTAGCCCTTAGATAAAACTGAGCAAGAGGCTTGGAGTATTTTCATG -----+-----+-----+-----+-----+-----+-----+ TGGATCGGAATCTATTTTGACTCGTTCTCCGAAACCTCATAAAGTAC T L A L D K T E Q E A L E Y F M	3120
3121	AAACAAATGAATGATGCACATCATGTGGCTGGACAACAAAAATGGAT -----+-----+-----+-----+-----+-----+-----+ TTTGTTTACTTACTACGTGTAGTACCAACCGACCTGTGTTTTTTACCTA K Q M N D A H H G G W T T K M D	3168
3169	TGGATCTTCCACACAATTAACAGCATGCATTGAACTGAAAGATAACT -+-----+-----+-----+-----+-----+-----+ ACCTAGAAGGTGTGTTAATTGTCGTACGTAACCTTGACTTTCCTATTGA W I F H T I K Q H A L N *	3216
3217	GAGAAATGAAAGCTCACTCTGGATTCCACACTGCACCTGTTAATAACT ---+-----+-----+-----+-----+-----+-----+ CTCTTTTACTTTCGAGTGAGACCTAAGGTGTGACGTGACAAATTATTGA	3264

+

3265	CTCAGCAGGCAAAGACCGATTGCATAGGAATTGCACAATCCATGAACA -----+-----+-----+-----+-----+-----+	3312
3266	GAGTCGTCCGTTTCTGGCTAACGTATCCTTAACGTGTAGGTACTTGT	
3313	GCATTAGATTACAGCAAGAACAGAAATAAAAATACTATATAATTAAA -----+-----+-----+-----+-----+-----+	3360
3314	CGTAATCTAAATGTCGTTCTTGCTTTATTTATGATATATATAAATTT	
3361	TAAATGTAAACGCAAACAGGGTTTGATAGCACCTAAACTAGTTCATTTC -----+-----+-----+-----+-----+-----+	3408
3362	ATTACATTTGCCGTTTGTCCTCCAAACTATCGTGAATTGATCAAGTAAAG	
3409	AAAA -+- -	3412
3410	TTTT	

FIG. 17A

hum110 1 ATGCCTCCAAGACCATCATCAGGTGAACCTGTGGGGCATCCACTTGATGCC 50
|||||
bov110 1 ATGCCTCCAAGACCATCATCAGGTGAACCTGTGGGGCATCCACTTGATGCC 50
51 CCAAGAATCCTAGTGAATGTTTACTACCAAAATGGAATGATAGTGACTT 100
|||||
51 CCAAGAATCCTAGTAGAATGTTTACTACCAAAATGGGATGATAGTGACTT 100
101 TAGAATGCCCTCCGTGAGGCTACATTAGTAACCTATAAAGCATGAACCTATTT 150
|||||
101 TAGAATGCCCTCCGTGAGGCTACGTTAATAACGATAAAGCATGAACCTATTT 150
151 AAAGAAGCAAGAAATACCCCTCTCCATCAACTTCTTCAAGATGAATCTTC 200
|||||
151 AAAGAAGCAAGAAATACCCCTCTCCATCAACTTCTTCAAGATGAATCTTC 200

FIG. 17B

201 TTACATTTTCGTAAGTGTACCCAAAGACAGAAAGGGAAGAAATTTTTC 250
|||||
201 TTACATTTTCGTAAGTGTACCCAAAGACAGAAAGGGAAGAAATTTTTC 250
|||||
251 ATGAAACAAGACGACTTTGTGATCTTCGGCCTTTTCAACCATTTTAAAA 300
|||||
251 ATGAAACAAGACGACTTTGTGACCTTCGGCCTTTTCAACCCCTTTTAAAA 300
|||||
301 GTAATTGAACCAAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAGAAAT 350
|||||
301 GTAATTGAACCAAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAGAAAT 350
|||||
351 TGGTTTTCGCTATCGGCATGCCAGTGTGCCGAATTTGATATGGTTAAAGATC 400
|||||
351 TGGTTTTCGCTATCGGCATGCCAGTGTGTGAATTCGATATGGTTAAAGATC 400
|||||
401 CTGAAGTACAGGACTTCCGAAGAAATATCTTAATGTTGTAAAGAAGCT 450
|||||
401 CAGAAGTACAGGACTTCCGAAGAAATATCTCAATGTTGTAAAGAAGCT 450

FIG. 17C

451 GTGGATCTTAGGGATCTTAATTACCTCATAGTAGAGCAATGTATGTCTA 500
|||||
451 GTGGATCTTAGGGATCTTAATTACCTCATAGTAGAGCAATGTATGTCTTA 500
|||||
501 TCCGCCACATGTAGAAATCTTCACCAGAGCTGCCAAAGCACATATATAATA 550
|||||
501 TCCTCCAAATGTAGAAATCTTCACCAGAACTGCCAAAGCACATATATAATA 550
|||||
551 AATTGGATAGAGGCCAAATAATAGTGGTGATTTGGTAATAGTTTCTCCA 600
|||||
551 AATTGGATAAAGGGCAATAATAGTGGTGATTTGGTAATAGTTTCTCCA 600
|||||
601 AATAATGACAAGCAGAAAGTATACTCTGAAAATCAACCATGACTGTGTGCC 650
|||||
601 AATAATGACAACAGAAAGTATACTCTGAAAATCAACCATGACTGTGTGCC 650
|||||
651 AGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGC 700
|||||
651 AGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGC 700
|||||

FIG. 17D

```
701 TATCATCTGAACAATTAAAACTCTGTGTTTGTAGAAATATCAGGGCAAGTAC 750
|||||
701 TATCATCTGAACAATAAACTCTGTGTTTGTAGAAATATCAGGGCAAGTAT 750

751 ATTTTAAAGTGTGGATGTGATGAATACTTCCTAGAAAAATATCCTCT 800
|||||
751 ATTTTAAAGTGTGGATGTGATGAATACTTCCTAGAAAAATATCCTCT 800

801 GAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGAGGATGCCCA 850
|||||
801 GAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGAGGATGCCCA 850

851 ATTTGAAGATGATGGCTAAAGAAAGCCCTTTATTCTCAACTGCCAATGGAC 900
|||||
851 ATTTGATGCTGATGGCTAAAGAAAGCCCTCTATTCTCAACTGCCAATGGAC 900

901 TGTTTTACAATGCCATCTTATTCAGACGCAATTCACAGCTACACCATA 950
|||||
901 TGTTTTACAATGCCATCATATTCAGACGCAATTCACAGCTACGCCATA 950
```

FIG. 17E

```
951 TATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCAC 1000
|||||
951 TATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCAC 1000

1001 TCAGAAATAAAAATCTTTGTGCAACCTACGTGAATCTAAATATTCGAGAC 1050
|||||
1001 TCAGAAATAAAAATCTTTGTGCAACCTATGTGAATGTAAATATTCGAGAC 1050

1051 ATTGACAAGATTTATGTTTCGAACAGGTATCTACCATGGAGGAGAACCCCTT 1100
|||||
1051 ATTGACAAGATTTATGTTTCGAACAGGTATCTACCATGGAGGAGAACCCCTT 1100

1101 ATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGA 1150
|||||
1101 ATGTGATAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGA 1150

1151 ATGAATGGCTGAATTATGATATATACATTCCCTCGATCTTCCTCGTGTGCT 1200
|||||
1151 ATGAATGGCTGAATTACGATATATACATTCCCTCGATCTTCCTCGTGTGCT 1200
```

FIG. 17F

1201 CGACTTTGCCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGTGCTAAAGA 1250
|||||
1201 CGACTTTGCCCTTTCCATTTGCTCTGTAAAGGCCGAAAGGTGCTAAAGA 1250
1251 GGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGTTGATTACACAG 1300
|||||
1251 GGAACACTGTCCATTGGCCTGGGAAATATAAACTTGTGTTGATTACACAG 1300
1301 ACACTCTAGTATCTGGAAAAAATGGCTTTGAAATCTTTGGCCAGTACCTCAT 1350
|
1301 ATACTCTAGTATCTGGAAAAAATGGCTTTGAAATCTTTGGCCAGTACCTCAT 1350
1351 GGATTAGAAGATTGTGCTGAACCCCTATTGGTGTGTTACTGGATCAAAATCCAAA 1400
|||
1351 GGACTAGAAGATTGTGCTGAACCCCTATTGGTGTGTTACTGGATCAAAATCCAAA 1400
1401 TAAAGAAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTCAGCAGTGTGG 1450
|||||
1401 TAAAGAAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTCAGCAGTGTGG 1450

11451	TAAAGTTCCCGAGATATGTCAGTGAATGAAGAGCATGCCAATTGGTCTGTA	1500
11451	TAAAGTTCCCGAGATATGTCAGTGAATGAAGAGCATGCCAATTGGTCTGTA	1500
11501	TCCCGAGAAAGCAGGATTTAGCTATTCCACGCAGGACTGAGTAACAGACT	1550
11501	TCCCGTGAAGCAGGATTTAGTTATTCCCATGCAGGACTGAGTAACAGACT	1550
11551	AGCTAGAGACAAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAA	1600
11551	AGCTAGAGACAAATGAATTAAGAGAAAATGATAAAGAACAGCTCCGAGCAA	1600
11601	TTTCTACACGAGATCCTCTCTCTGAAATCACTGACGAGAGAAAGATTTT	1650
11601	TTTGTACACGAGATCCTCTATCTGAAATCACTGAGCAAGAGAAAAGATTTT	1650
11651	CTATGGAGTCACAGACACTATTGTGTAACCTATCCCCGAAATCTACCCAA	1700
11651	CTGTGGAGCCACAGACACTATTGTGTAACCTATCCCCGAAATCTACCCAA	1700

FIG. 17H

```
1701 ATTGCTTCTGTCTGTTAAATGGAATTCTAGAGATGAAGTAGCCAGATGT 1750
|||||
1701 ATTGCTTCTGTCTGTTAAATGGAACTCTAGAGATGAAGTAGCTCAGATGT 1750

1751 ATTGCTTGGTAAAGATTTGGCCTCCAATCAAACCTGAACAGGCTATGGAA 1800
|||||
1751 ACTGCTTGGTAAAGATTTGGCCTCCAATCAAAGCCTGAACAGGCTATGGAG 1800

1801 CTTCTGGACTGTAAATTACCCAGATCCTATGGTTTCGAGGTTTGTGCTTTCG 1850
|||||
1801 CTTCTGGACTGCAATTACCCAGATCCTATGGTTTCGAGGTTTGTGCTTTCG 1850

1851 GTGCTTGGAAAAAATATTTAACAGATGACAAAACCTTCTCAGTATTTAATTC 1900
|||||
1851 GTGCTTAGAAAAAATATTTAACAGATGACAAAACCTTCTCAGTACCTAATTC 1900

1901 AGCTAGTACAGGTCCTAAAAATATGAACAATATTGGATAACTGCTTGTG 1950
|||||
1901 AGCTAGTACAGGTACTAAAAATATGAACAGTATTGGATAACCTGCTTGTG 1950
```

FIG. 171

```
1951 AGATTTTACTGAAGAAAGCATTGACTAATCAAAGGATTGGGCACCTTTT 2000
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1951 AGATTTTACTCAAAAAGCGTTAACTAATCAAAGGATCGGTCACCTTTT 2000

2001 CTTTGGCATTAAATCTGAGATGCACAATAAAACAGTTAGCCAGAGGT 2050
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2001 CTTTGGCATTAAATCTGAGATGCACAATAAAACAGTTAGTCAGAGGT 2050

2051 TTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTATTGAAG 2100
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2051 TTGGCCTGCTTTTGGAGTCCTATTGCCGTGCATGTGGGATGTATCTGAAG 2100

2101 CACCTGAATAGGCAAGTCGAGGCAATGGAAGCTCATTAACCTTAAGTGA 2150
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2101 CACCTTAATAGGCAAGTTGAGGCTATGGAAGCTCATTAACCTTGACTGA 2150

2151 CATTCTCAAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGT 2200
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2151 CATTCTCAAAACAGAGAGAAGGATGAAACACAAAAGGTACAGATGAAGT 2200
```


FIG. 17J

2201 TTTTAGTTGAGCAAAATGAGGCGACAGATTTTCATGGATGCCCTACAGGGC 2250
|||||
2201 TTTTAGTTGAGCAAAATGCGGCGACAGATTTTCATGGATGCTCTCCAGGGC 2250
|||||
2251 TTGCTGTCTCCTCTAAACCCCTGCTCATCAACTAGGAAACCTCAGGCTTAA 2300
||
2251 TTTCTGTCTCCTCTAAACCCCTGCTCATCAGCTGGGAAATCTCAGGCTTGA 2300
|||||
2301 AGAGTGTGCGAATTATGTCTTCTGCAAAAGGCCACTGTGGTTGAATTGGG 2350
|||||
2301 AGAGTGTGCGAATTATGTCTTCTGCAAAAGGCCACTGTGGTTGAATTGGG 2350
|||||
2351 AGAAGCCAGACATCATGTCTCAGAGTTACTGTTTCAGAAACAATGAGATCATC 2400
|||||
2351 AGAAGCCAGACATCATGTCTCAGAAATTACTCTTTCAGAAACAATGAGATCATC 2400
|||||
2401 TTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATTAT 2450
|||||
2401 TTTAAAAATGGGGATGATTACGGCAAGATATGCTAACCCCTTCAGATTAT 2450

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2451	TCGTATTATGGAAAATATCTGGCAAAATCAAGGCTTGTGATCTTCGAATGT	2500
2451	TCGCATTATGGAAAATATCTGGCAAAATCAAGGCTTGTGATCTTCGAATGT	2500
2501	TACCTTATGGTTGCTGTCTCAATCGGTGACTGTGTGGACTTATTGAGGTG	2550
2501	TACCTTATGGATGCTGTCTCAATCGGTGACTGTGTGGACTTATCGAGGTG	2550
2551	GTCCGAAATTCTCACACTATTATGCAAAATTCAGTGC AAAAGCGGCTTGAA	2600
2551	GTGAGAAATTCTCACACTATAATGCAGATTCAGTGTAAAGGAGGCCCTGAA	2600
2601	AGGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGGCTCAAAGACA	2650
2601	AGGTGCACTGCAGTTTAAACAGCCACACACTCCATCAGTGGCTCAAAGACA	2650
2651	AGAACAAAGGAGAAAATATATGATGCAGCCATTGACCTGTTACACGTTCA	2700
2651	AGAACAAAGGGGAAATATATGATCGGCCATCGATTGTTTACACGATCA	2700

FIG. 17L

2701 TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCA 2750
|||||
2701 TGTGCTGGATAATTGTGTGCCACCTTCATTTTGGGAATTGGAGATCGTCA 2750
|||||
2751 CAATAGTAACATCATGTGTAAGACGATGGACAACCTGTTTCATATAGATT 2800
|||||
2751 CAATAGTAATATCATGGTTAAAGATGATGGACAACCTGTTTCATATAGATT 2800
|||||
2801 TTGGACACTTTTGGATCACAAAGAAAGAAAATTTGGTTATAAACGAGAA 2850
|||||
2801 TTGGACACTTTTGGATCACAAAGAAAGAAAATTTGGTTATAAACGAGAG 2850
|||||
2851 CGTGTGCCATTGTGTTTGACACAGGATTCTTAATAGTGATTAGTAAAGG 2900
||
2851 CGCGTGCCGTTGTGTTTGACACAAAGATTCTTAATAGTGATTAGTAAAGG 2900
|||||
2901 AGCCCAAGAATGCACAAAGACAAAGAGAAATTGAGAGGTTTCAGGAGATGT 2950
|||||
2901 AGCCCAAGAATGCACAAAGACAAAGAGAAATTGAGAGGTTTCAGGAGATGT 2950
|||||

FIG. 17M

2951 GTTACAAGGCTTATCTAGCTATTGACAGCATGCCAATCTCTTCATAAAAT 3000
|||||
2951 GTTACAAGGCTTATCTAGCTATTGCGCAGCATGCCAATCTCTTCATAAAAT 3000
|||||
3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGA 3050
|||||
3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTGCAATCTTTTGA 3050
|||||
3051 TGACATTGCATACATTGGAAGACCCCTAGCCTTAGATAAAACTGAGCAAG 3100
|||||
3051 TGATATTGCATACATTGGAAGACCCCTAGCCTTAGATAAAACTGAGCAAG 3100
|||||
3101 AGGCTTTGGAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGC 3150
|||||
3101 AGGCTTTGGAGTATTTTCATGAAACAAATGAATGATGCACACCATGGTGGC 3150
|||||
3151 TGGACAACAAAATGGATTGGATCTTCCACACAAATTAACAGCATGCATT 3200
|||||
3151 TGGACAACAAAATGGATTGGATCTTCCACACAAATTAAGCAGCATGCTTT 3200
|||||
3201 GAACTGAAAGATAAAGTGAAGAAATGAAAGCTCACTCTGTGA
|||||
3201 GAACTGA.....

+

h	MPPRPSSGELWGIHLMPPRILVECLLPNGMIVTLECLREATLVTIKHELFKEARKYPLHQ	10	20	30	40	50	60
b		10	20	30	40	50	60
h	LLQDESSYIFVSVTQEAEREFFDETRRLCDLRLFQPFCLKVIEPVGNREEKILNREIGFA	70	80	90	100	110	120
b		70	80	90	100	110	120
h	IGMPVCEFDVMKDPEVQDFRRNILNVCKEAVDLRDLNSPHSRAMYVYPHVESSELPHK	130	140	150	160	170	180
b		130	140	150	160	170	180

```

190      200      210      220      230      240
h IYNKLDRGQII VVIWIVSPNNDKQKYTLKINHDCVPEQVIAEAIRKKTRSMLLSSEQLK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
b IYNKLDKGQII VVIWIVSPNNDKQKYTLKINHDCVPEQVIAEAIRKKTRSMLLSSEQLK
190      200      210      220      230      240

250      260      270      280      290      300
h LCVLEYQGKYILKVCGCDEYFLEKYPLSQKYIRSCIMLGRMPNLKMMAKESLYSQLPMD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
b LCVLEYQGKYILKVCGCDEYFLEKYPLSQKYIRSCIMLGRMPNLMLMAKESLYSQLPMD
250      260      270      280      290      300

310      320      330      340      350      360
h CFTMPSYSRRISTATPYMNGETSTKSLWVINRALRIKILCATYVNLNIRDIDKIYVRTGI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
b CFTMPSYSRRISTATPYMNGETSTKSLWVINSALRIKILCATYVNVNIRDIDKIYVRTGI
310      320      330      340      350      360

```

FIG. 18C

h	YHGGEPLCDNVNTQ	RVPCSNPRWNEWLN	YDIYIPDL	PRAARLCL	SICSVKGRKGAKEEHC	420
						410
b	YHGGEPLCDNVNTQ	RVPCSNPRWNEWLN	YDIYIPDL	PRAARLCL	SICSVKGRKGAKEEHC	420
						410
h	PLAWGNINLFDYTD	TLVSGKMA	NLWPVPHGLE	LLNP	IGVTGSNPNKETPCLELEFDWF	480
						470
b	PLAWGNINLFDYTD	TLVSGKMA	NLWPVPHGLE	LLNP	IGVTGSNPNKETPCLELEFDWF	480
						470
h	SSVVKFPDMSVIEE	HANWSVSREAGFS	YSHAGLSNRL	ARDNEL	RENDKEQLKAISTRDPL	540
						530
b	SSVVKFPDMSVIEE	HANWSVSREAGFS	YSHAGLSNRL	ARDNEL	RENDKEQLRAICTRDPL	540
						530

FIG. 18D

550	560	570	580	590	600
h	SEITEQEKDFLWSHRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCLVKDWPP	IKPEQAME			
b	SEITEQEKDFLWSHRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCLVKDWPP	IKPEQAME			
550	560	570	580	590	600
610	620	630	640	650	660
h	LLDCNYPDPMVRGFAVRCLEKYLTDCLKLSQYLIQLVQLKYEQYLDNLLVRFLLK	KALTN			
b	LLDCNYPDPMVRGFAVRCLEKYLTDCLKLSQYLIQLVQLKYEQYLDNLLVRFLLK	KALTN			
610	620	630	640	650	660
670	680	690	700	710	720
h	QRIGHFFFWHLKSEMHNKTVSQRFGLLLESYCRACGMYLKHNLNRQVEAMEK	LINLTDILK			
b	QRIGHFFFWHLKSEMHNKTVSQRFGLLLESYCRACGMYLKHNLNRQVEAMEK	LINLTDILK			
670	680	690	700	710	720

FIG. 18E

730	740	750	760	770	780
h	QERKDETQKVQMKFLVEQMRPPDFMDALQGLLSPLNPAHQQLGNLRLKECRIMSSAKRPLW				
	:				
b	QEKKDETQKVQMKFLVEQMRPPDFMDALQGLLSPLNPAHQQLGNLRLKECRIMSSAKRPLW				
730	740	750	760	770	780
790	800	810	820	830	840
h	LNWENPDIMSELLFQNNNEIIFKNGDDLRRQDMLTLQIIRIMENIWQNQGLDLRMLPYGCLS				
b	LNWENPDIMSELLFQNNNEIIFKNGDDLRRQDMLTLQIIRIMENIWQNQGLDLRMLPYGCLS				
790	800	810	820	830	840
850	860	870	880	890	900
h	IGDCVGLIEVVRNSHTIMQIQCKGGLKGALQFNSHTLHQWLKDKNKG E IYDAAIDLFTRS				
b	IGDCVGLIEVVRNSHTIMQIQCKGGLKGALQFNSHTLHQWLKDKNKG E IYDAAIDLFTRS				
850	860	870	880	890	900

FIG. 18F

h	910	920	930	940	950	960
	CAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVPFVLTQDF					
b	910	920	930	940	950	960
	CAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVPFVLTQDF					
h	970	980	990	1000	1010	1020
	LIVISKAQECTKTREFEFQEMCYKAYLAIRQHANLFINLFSMMLGSGMPPELQSFDDIA					
b	970	980	990	1000	1010	1020
	LIVISKAQECTKTREFEFQEMCYKAYLAIRQHANLFINLFSMMLGSGMPPELQSFDDIA					
h	1030	1040	1050	1060	1070	1080
	YIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTIKQHALNXXKITEKMKAHSG					
b	1030	1040	1050	1060		
	YIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTIKQHALNX					

FIG. 19A

1 MPPRPSSGEL WGIHLMPPRI LVECLLPNGM IVTLECLREA TLVTIKHELF
51 KEARKYPLHQ LLQDESSYIF VSVTQEAERE EFFDETRRLC DLRLFQPFLLK
101 VIEPVGNREE KILNREIGFA IGMPVCEEDM VKDPEVQDFR RNILNVCKEA
151 VDLRDINSPH SRAMYVYPFH VESSPELPKH IYNKLDRGQI IVVIWVIVSP
201 NNDKQKYTLK INHDCVPEQV IAEAIRKKTR SMLLSSEQLK LCVLEYQGY
251 ILKVCGCDEY FLEKYPLSQY KYIRSCIMLG RMPNLKMMAK ESLYSQLPMD
301 CFTMPSYSRR ISTATPYMNG ETSTKSLWVI NRALRIKILC ATYVNLNIRD
351 IDKIYVRTGI YHGGEPLCDN VNTQRVPCSN PRWNEWLNVD IYIPDLPRAA
401 RLCLSICSVK GRKGAKKEHC PLAWGNINLF DYTDTLVSGK MALNLWPVPH
451 GLEDLINPIG VTGSNPKNKET PCLELEFDWF SSVVKFPDMS VIEEHANWSV

FIG. 19B

501 SREAGFSYSH AGLSNRLARD NELRENDKEQ LKAISTRDPL SEITEQEKDF
551 LWSHRHYCVT IPEILPKLLL SVKWSRDEV AQMYCLVKDW PPIKPEQAME
601 LLDCNYPDPM VRGFAVRCL E KYLTDDKLSQ YLIQLVQVLK YEQYLDNLLV
651 RFLKKALTN QRIGHFFFWH LKSEMHNKT V SQFGLLES YCRACGYLK
701 HLN RQVEAME KLINLT DILK QERKDETQKV QMKFLVEQMR RPDFMDALQG
751 LLSPLNPAHQ LGNLR LKECR IMSSAKRPLW LN WENPDIMS ELLFQNN EII
801 FKN GDDL RQD MTLQIIRIM ENIWQNGLD LRMLPYGCLS IGDCVGLIEV
851 VRNSHTIMQI QCKGGLKGAL QFN SHTLHQW LKDKNKGEIY DAAIDL FTRS
901 CAGYCVATFI LGIGDRHNSN IMVKDDGQLF HIDFGHLDH KKKKFGYKRE
951 RVPFVLTQDF LIVISKGAQE CTKTREFFERF QEMCYKAYLA IRQHANLFIN
1001 LFSMMLGSGM PELQSFDDIA YIRKTLALDK TEQEALEYFM KOMNDAHGG
1051 WTTKMDWIFH TIKQHALN*

FIG. 20

1 GGAGACGACTTGGACAGGATCAACTTATTCTTCAAATCATTTCACTC
GlyAspAspLeuArgGlnAspGlnLeuIleLeuGlnIleIleSerLeu

49 ATGGACAAGCTGTTACGGAAAGAAATCTGGACTTGAAATTGACACCT
MetAspLysLeuLeuArgLysGluAsnLeuAspLeuLysLeuThrPro

97 TATAAGGTGTAGCCACCAGTACAAAACATGGCTTCATGCAGTTTATC
TyrLysValLeuAlaThrSerThrLysHisGlyPheMetGlnPheIle

145 CAGTCAGTtCCTGTGGCTGaaGTTCTTGATACAGAGGGAAGCATTTCAG
GlnSerValProValAlaGluValLeuAspThrGluGlySerIleGln

193 AACTTTTTTAGAAAAATATGCACCAAGTGAGAATGGCCAAATGGGATT
AsnPhePheArgLysTyrAlaProSerGluAsnGlyProAsnGlyIle

241 AGTGCTGAGGTCATGGACACTtACGTTAAAGCTGTGCTGGATATTGC
SerAlaGluValMetAspThrTyrValLysSerCysAlaGlyTyrCys

289 GTGATCACCTATATACTTGGAGTTGGAGACAGGCACCTGGATAACCTT
ValIleThrTyrIleLeuGlyValGlyAspArgHisLeuAspAsnLeu

337 TTGCTAACCAAAACAGGCAAACTCTCCACATCGATTTCGGCCAC
LeuLeuThrLysThrGlyLysLeuPheHisIleAspPheGlyHis

FIG. 21

1 GGGATGACTTACGGCAGGACATGCTAACGCTGCAGATGATTCGCATC
GlyAspAspLeuArgGlnAspMetLeuThrLeuGlnMetIleArgIle

49 ATGAGCAAGATCTGGGTCCAGGAGGGGCTGGACATGCGCATGGTCATC
MetSerLysIleTrpValGlnGluGlyLeuAspMetArgMetValIle

97 TTCCGCTGCTTCTCCACCGCCGGGCGGAGGATGGTGGAGATGATC
PheArgCysPheSerThrGlyArgGlyArgGlyMetValGluMetIle

145 CCTAATGCTGAGACCCCTGCGTAAGATCCAGGTGGAGCATGGGGTGACC
ProAsnAlaGluThrLeuArgLysIleGlnValGluHisGlyValThr

193 GGCTCGTTCAAGGACCGCCCTGGCAGACCGGCTGCAGAAACACAAC
GlySerPheLysAspArgProLeuAlaAspArgLeuGlnLysHisAsn

241 CCTGGGAGGACGAGTATGAGAAGGCTGTGGAACTTTATCTACTCC
ProGlyGluAspGluTyrGluLysAlaValGluAsnPheIleTyrSer

289 TGGCTGGCTGCTGCGTGGCCACGTACGTCTTGGGCATCTGTGACCga
CysAlaGlyCysCysValAlaThrTyrValLeuGlyIleCysAspArg

337 CATAATGACAACATCATGCTGAAGACCACCTGGTCACATGTTCCACATC
HisAsnAspAsnIleMetLeuLysThrThrGlyHisMetPheHisIle

385 GACTTCGGC
AspPheGly

+

1

vps34	GDDL	RQDqLv	QIIsl	Mnell	knEnv	DLkLt	Pyki	LaT	Gp	qeGa	IE	fIpN	50
PITR-c	GDDL	RQDqLi	LQIIsl	Mdkll	rkEn	LDLkLt	Pykv	LaT	stkh	G	Fmqf	Iqs	
hump110	GDDL	RQDmLt	LQIIri	Meni	wnqng	LDLr	MLPY	gCLsi	Gdcv	GLIE	Vv	Rn	
PITR-f	GDDL	RQDmLt	LQmIri	Mski	wvqE	gLDm	rMvi	FrcF	stGr	grGM	VE	mIpN	
Consensus	GDDL	RQD-L	-LQII	-M-----	E-LDL	---PY--	L-TG	---G-IE	-I-N				
51													100
vps34	dtla	silsky	hGi	L	gy.....	Lkl	hypde	Na	tlg	Vq	gw	lDn	FVksCA
PITR-c	vpva	e	l	dt	egsI	qn	f.....	Frk	Yap	se	Ng	pngI	saevmDtYVksCA
hump110	shtim	qi	qckg	GLk	Gal	qfn	sh	tLh	qWl	kdk	Nk	ge..Iy	daaiDLftrSCA
PITR-f	aetl	rki	qveh	G	Vt	Gs..	fkd	rpL	ad	rLq	khN	pge	deyekavEnFIySCA
Consensus	-----	GI	-G	-----	L-----	N-----	I-----	D-FV	-SCA				
101													133
vps34	GYC	V	iTY	ILG	V	G	<u>DR</u>	<u>HD</u>	<u>N</u>	<u>LL</u>	<u>vt</u>	<u>pd</u>	GhFFHa <u>DFG</u>
PITR-c	GYC	V	iTY	ILG	V	G	<u>DR</u>	<u>HD</u>	<u>N</u>	<u>LL</u>	<u>tk</u>	GkLFHID <u>FG</u>	
hump110	GYC	V	aT	FIL	G	<u>IG</u>	<u>DR</u>	<u>H</u>	<u>n</u>	<u>Ni</u>	<u>Mv</u>	<u>kd</u>	GqLFHID <u>FG</u>
PITR-f	GCC	V	aTY	VL	G	<u>IC</u>	<u>DR</u>	<u>H</u>	<u>D</u>	<u>Ni</u>	<u>ML</u>	<u>kt</u>	GhMFHID <u>FG</u>
Consensus	GYC	V	-TY	ILG	-G	<u>DR</u>	<u>H</u>	-D	<u>N</u>	-----	G-LFHID	<u>FG</u>	

FIG. 23A

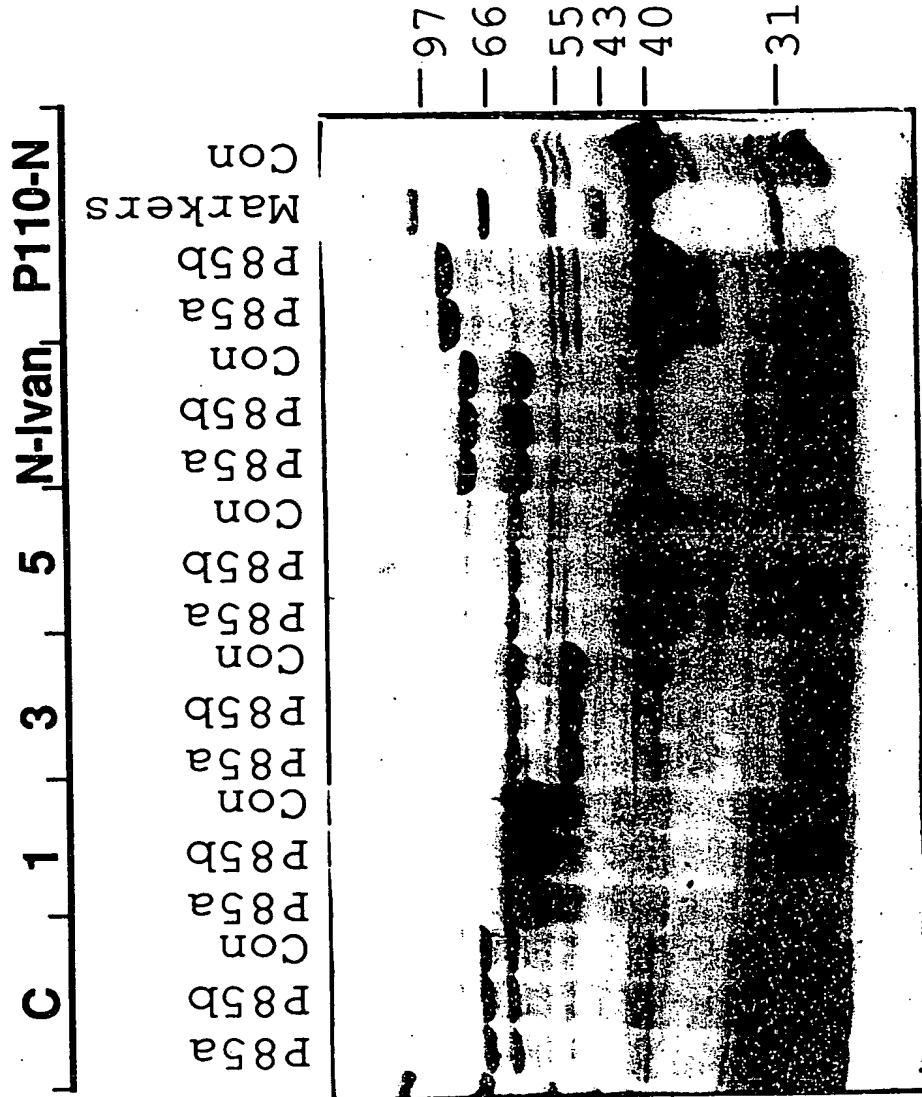


FIG. 23B

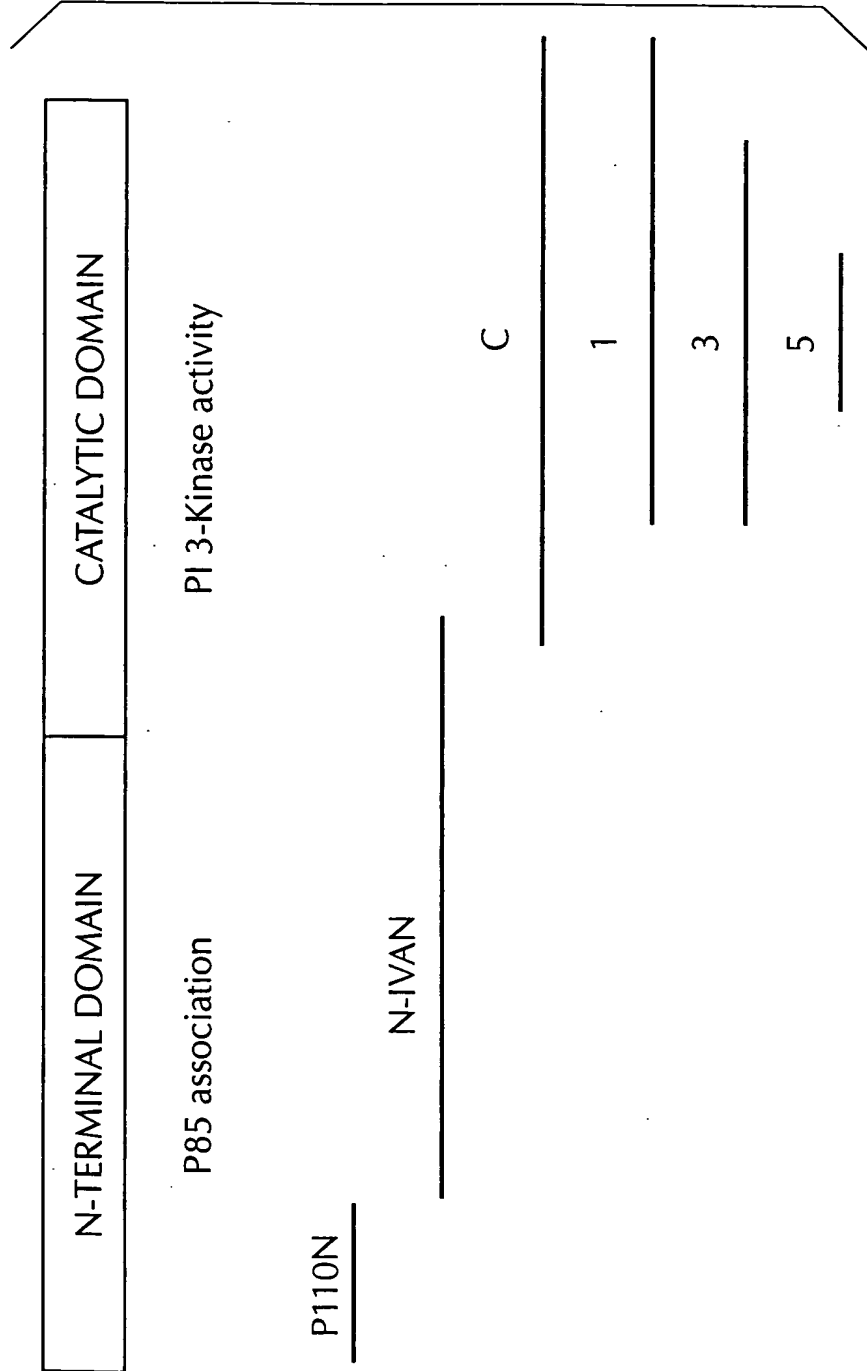


FIG. 24

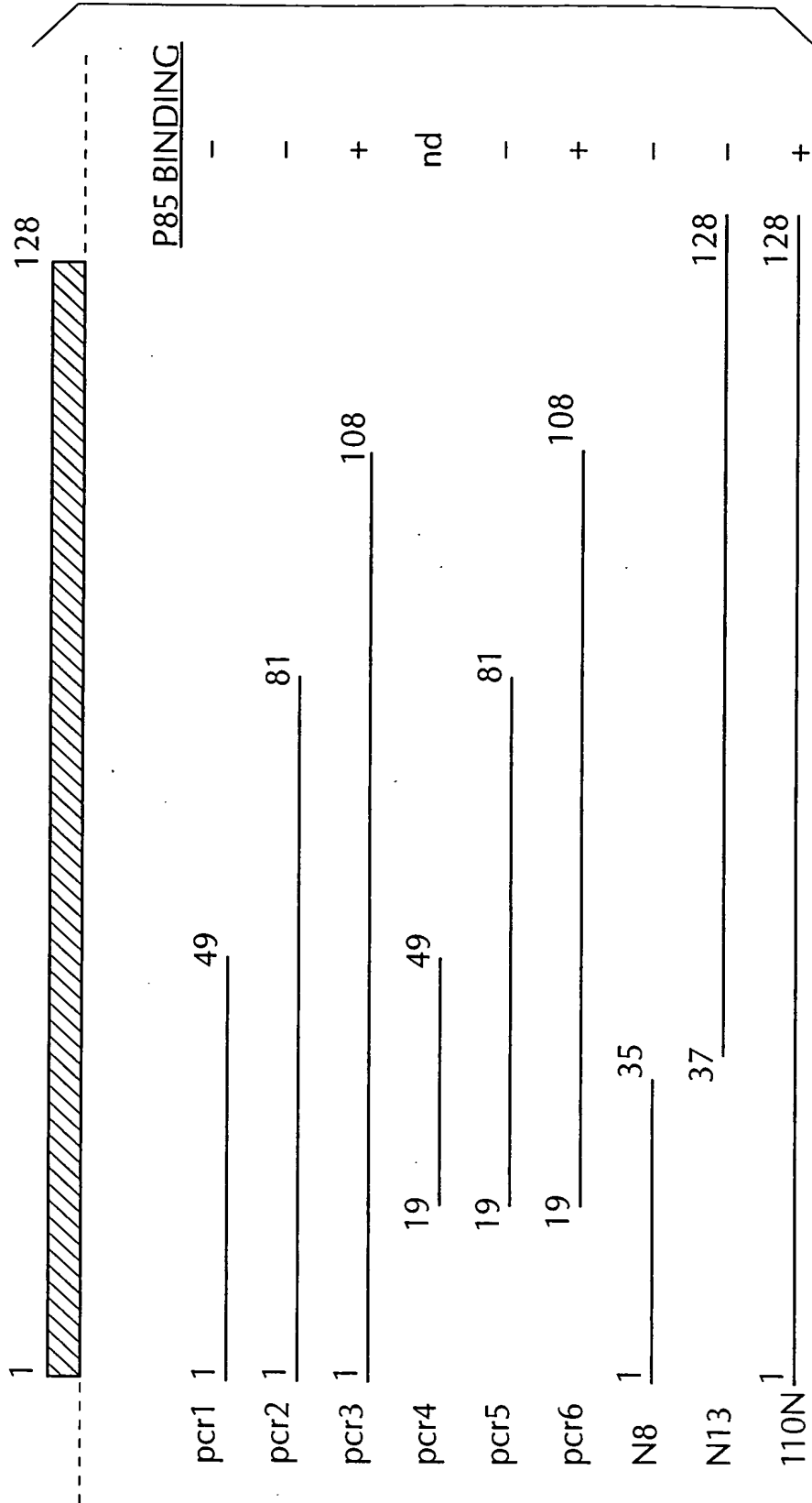


FIG. 25A

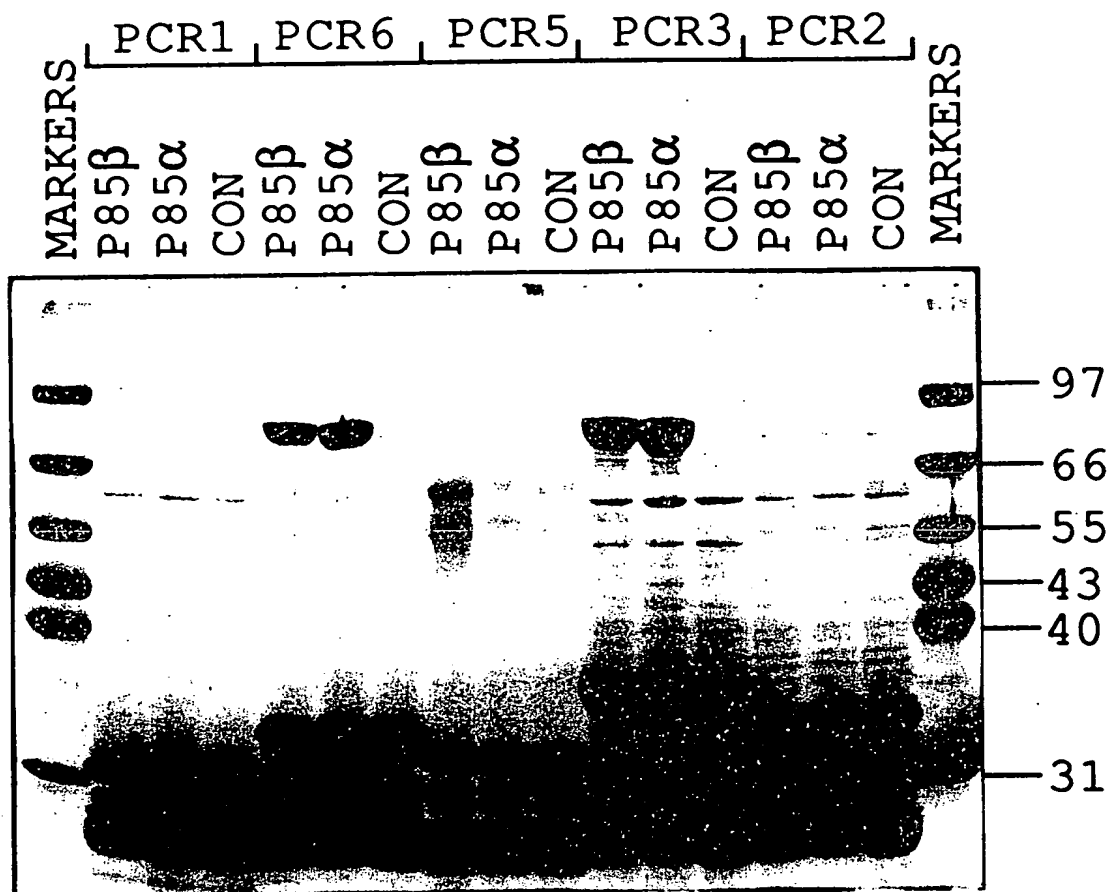


FIG. 25B

